

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representation of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
  - TEXT CUT OFF AT TOP, BOTTOM OR SIDES
  - FADED TEXT
  - ILLEGIBLE TEXT
  - SKEWED/SLANTED IMAGES
  - COLORED PHOTOS
  - BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- 
- GRAY SCALE DOCUMENTS

## **IMAGES ARE BEST AVAILABLE COPY**

**As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/12, C07K 14/705, 16/28, C12N 5/10, G01N 33/68</b>	<b>A1</b>	<b>(11) International Publication Number:</b> <b>WO 99/29847</b> <b>(43) International Publication Date:</b> 17 June 1999 (17.06.99)
<b>(21) International Application Number:</b> PCT/US98/23161 <b>(22) International Filing Date:</b> 30 October 1998 (30.10.98)  <b>(30) Priority Data:</b> 08/985,809 5 December 1997 (05.12.97) US  <b>(71) Applicant (for all designated States except US):</b> LOYOLA UNIVERSITY OF CHICAGO [US/US]; 2160 South First Avenue, Maywood, IL 60153 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> PEREZ-REYES, Edward [US/US]; 320 South Birchwood Drive, Naperville, IL 60540 (US). CRIBBS, Leanne, L. [US/US]; 1737 North Natoma, Chicago, IL 60707 (US).  <b>(74) Agents:</b> HEFNER, M., Daniel et al.; Leydig, Voit & Mayer, Ltd., Suite 4900, Two Prudential Plaza, 180 North Stetson, Chicago, IL 60601-6780 (US).		<b>(81) Designated States:</b> CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> With international search report.
<b>(54) Title:</b> T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF USING SAME  <b>(57) Abstract</b> <p>The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.</p>		

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LJ	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

## T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF USING SAME

### STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

This invention was made with Government support under Grant Number HL58728 awarded by the National Heart, Lung, and Blood Institute of the National Institutes of Health. The United States Government may have certain rights in this invention.

### TECHNICAL FIELD OF THE INVENTION

The present invention relates to cloned T-type calcium channels.

### BACKGROUND OF THE INVENTION

Biological membranes are themselves generally impermeable to ionic species. Thus, ions enter cells through regulated pores formed from membrane-associated proteins. Most of these regulated pores are voltage-dependent and are thus able to transduce changes in the transmembrane potential into ion flux. Voltage-gated ion channels form a "superfamily" of related proteins (cf. Jan et al., *Nature*, 345, 672 (1990)). Peculiar to this genus is a high degree of conservation in molecular structure. Generally, voltage-gated channels are membrane bound glycosylated proteins formed of many subunits. Large  $\alpha$  subunits form a pore in the membrane that is selective for a given ionic species. Each  $\alpha$  subunit contains four domains (I, II, III, and IV). Each channel domain has six putative transmembrane helical segments ( $S_1$ - $S_6$ ). In general, the segments within each domain are similar but not identical. Aside from overall structural conservation, certain charged residues within the domains are highly conserved among voltage-gated ion channels (Jan et al., *supra*; Stühmer et al., *Nature*, 339, 597-603 (1989)).

Differences in charged residues between groups of voltage-gated ion channels confer properties unique to each subgroup, such as ion selectivity. For example, most voltage gated ion channels are selective for either sodium, potassium or calcium. Known calcium channels require a ring of negative charge provided by glutamate residues found at similar locations in each of the domains (Yang et al., *Nature*, 366, 158-61 (1993)).

Voltage-gated channels are often classified on the basis of their electrophysiology. The resting membrane potential of most animal cells is between about -70 mV and -80 mV. When the membrane becomes depolarized (moved towards 0 mV), various membrane channels become activated (they are said to

“open”). Thus, one basis for classifying membrane channels is the membrane potential necessary to activate (or “gate”) them (voltage dependency). For example, “T-type” calcium channels are activated at a lower voltage than L- or N-type channels (Nowycky et al., *Nature*, 316, 440-43 (1985)). Other physiological properties are the activation kinetics, inactivation kinetics, tail current (deactivation kinetics), and single channel conductance. Thus, in comparison to other calcium currents, T-type calcium current is characteristically short (Chen et al., *J. Gen. Physiol.*, 96, 603-30 (1990)), and it exhibits characteristically slow activation kinetics near threshold, fast inactivation kinetics, and slow tail current (Randall et al., *Neuropharmacol.*, 63, 879-93 (1997); Carbone et al., *Nature*, 310, 501-02 (1984); Nilius et al., *Nature*, 316, 443-46 (1985)).

Calcium currents have been implicated in many neurological and muscular functions. For example, T-type calcium current is associated with cardiac pacemaker activity, pain transmission in the central nervous system, and in other physiological functions. Defects in T-type calcium current have been implicated in cardiac arrhythmia, hypertension, and epilepsy. Given their potential clinical value, the pharmacological properties of calcium channels have been the subject of extensive study. Most such studies have involved L-type channels because, unlike T-type channels, L-type calcium channels are readily purified from cell extracts. For example, L-type calcium channels have been purified using dihydropyridine drugs (e.g., nifedipine) which can bind with sufficiently high affinity to serve as a ligand for purifying L-type calcium channels. Such purified and cloned L-type calcium channels have been used to develop assays for drugs affecting L-type calcium channels (see, e.g., U.S. Patents 5,429,921 and 5,386,025).

While many electrophysiological characteristics of T-type calcium currents are known, the lack of isolated T-type channels has stalled research into the pharmacology and biophysics underlying the T-type calcium current, at least in comparison with other calcium channels. Indeed, while it is generally assumed that voltage-sensitive ion channels are responsible for the current, no such channel protein, nor any nucleic acid encoding such a protein, has been isolated. In view of the foregoing problems, there exists a need for an isolated T-type calcium channel and a nucleic acid encoding a T-type calcium channel.

### BRIEF SUMMARY OF THE INVENTION

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or

substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

The present invention is useful for exploring the electrophysiology and pharmacology of the T-type calcium current. Such knowledge can lead to the development of drugs for potentiating or attenuating T-type calcium channels. Thus, the present invention provides an assay for identifying potential drugs affecting T-type calcium channels by exposing cells expressing a T-type calcium channel to a putative drug and then measuring the calcium flux in response to a change in membrane potential. The identification of drugs affecting T-type calcium channels will facilitate even greater understanding of the biophysics of these proteins. Furthermore, some such drugs could have potential clinical applications.

The invention can best be understood with reference to the accompanying drawings and in the following detailed description of the preferred embodiments.

## BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E compare the complete amino acid sequences of three types of T-type calcium channels ( $\alpha 1G$  (or  $Ca_vT.1$ ),  $\alpha 1H$  (or  $Ca_vT.2$ ), and  $\alpha 1I$  (or  $Ca_vT.3$ )), indicating conserved functional domains.

Figures 2A-2D are graphic representations of the current-voltage relationships of three cloned T-type calcium channels (Figures 2A, 2B, and 2C) and a cloned R-type calcium channel (Figure 2D).

Figure 3A is a graphic representation of the average current-voltage curve for cloned T-type calcium channels ( $\alpha 1G$ , triangles,  $\alpha 1H$ , inverted triangles,  $\alpha 1I$ , circles), and a cloned R-type calcium channel (filled squares). Figure 3B compares the normalized conductance of a cloned T-type calcium channel at three different concentrations of  $BaCl_2$ .

Figure 4 depicts average kinetics of the tail current as a function of repolarization potential for  $\alpha 1G$  (triangles),  $\alpha 1H$  (inverted triangles),  $\alpha 1I$  (circles), and a cloned R-type calcium channel (filled squares).

Figures 5A and 5B graphically present data concerning the use of a cloned T-type calcium channel to detect drugs affecting the channel. Figure 6A depicts the effect of 100  $\mu M$  on current-voltage relationships with a single dosage of mibefradil. Figure 6B illustrates the effect on T-type channel conductance of various doses of mibefradil.

## DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel  $\alpha$

subunit. The nucleic acid can be of any type, and it can include other elements aside from a sequence encoding a T-type calcium channel domain or domains. For example, where the nucleic acid comprises RNA, it can also include regulatory sequences suitable to permit translation of the RNA. Thus, an RNA nucleic acid of  
5 the present invention preferably has at least one ribosome entry site, and preferably has a polyadenosine tail for stabilizing the RNA in the cellular environment.

Similarly, DNA nucleic acids of the present invention can have regulatory elements for promoting the transcription of sequence encoding the T-type calcium channel into an RNA such as that described above. For example, a DNA nucleic acid of the  
10 present invention can have a promoter and/or an enhancer sequence. While the nucleic acid can be any type of nucleic acid, the nucleic acid preferably comprises a cDNA. A cDNA nucleic acid is preferred over other nucleic acids to permit the nucleic acid to be readily cloned, sequenced, and expressed in a wide variety of cells.

The choice of promoter and/or an enhancer will largely depend on the milieu in  
15 which the nucleic acid is to be expressed. Thus, for expression in bacterial cells, the regulatory elements are bacterial promoters. Similarly, for expression in mammalian cells, the regulatory elements are able to effect expression in mammalian cells. While many such regulatory elements are known in the art, examples include prokaryotic promoters and viral promoters (e.g., retroviral ITRs, LTRs, immediate early viral  
20 promoters (IEp), such as herpesvirus IEp (e.g., ICP4-IEp and ICP0-IEp), cytomegalovirus (CMV) IEp, and other viral promoters, such as Rous Sarcoma Virus (RSV) promoters, and Murine Leukemia Virus (MLV) promoters). Other suitable promoters are eukaryotic promoters, such as enhancers (e.g., the rabbit  $\beta$ -globin regulatory elements), constitutively active promoters (e.g., the  $\beta$ -actin promoter, etc.),  
25 signal specific promoters (e.g., inducible promoters such as a promoter responsive to RU486, etc.), and tissue-specific promoters (e.g., those active in epidermal tissue, dermal tissue, tissue of the digestive organs (e.g., cells of the esophagus, stomach, intestines, colon, etc., or their related glands), smooth muscles, such as vascular  
30 smooth muscles, cardiac muscles, skeletal muscles, lung tissue, hepatocytes, lymphocytes, endothelial cells, sclerocytes, kidney cells, glandular cells (e.g., those in the thymus, ovaries, testicles, pancreas, adrenals, pituitary, etc.), tumor cells, cells in connective tissue, cells in the central nervous system (e.g., neurons, neuralgia, etc.), cells in the peripheral nervous system, and other cells of interest).

The isolated or substantially purified nucleic acid of the present invention  
35 encodes all or part of a T-type calcium channel  $\alpha$  subunit. As used herein, a "calcium channel" includes a protein structure for facilitating the flux of calcium ions across a biological membrane into which the calcium channel is inserted. As used herein, a "T-type channel" is a type of voltage-gated ion channel that facilitates the flux of ions



when the membrane potential of a biological membrane into which it is inserted experiences a slight depolarization. Thus, a T-type calcium channel can begin to gate from about -60 mV to about -30 mV (i.e., about -45 mV to about -35 mV) in about 10 mM  $Ba^{2+}$ . Additionally, T-type channels of the present invention exhibit a slow  
5 deactivation (tail current) following depolarization. Thus, a T-type calcium channel can exhibit a tail current that decays exponentially with a tau value from about 1 ms to about 10 ms (e.g., from about 4 ms to about 7 ms, such as about 6 ms) following repolarization to a membrane potential from about -80 mV to about -60 mV in a solution with a  $Ba^{2+}$  concentration of from about 10 mM to about 40 mM. Another  
10 defining characteristic of T-type calcium channels is that they exhibit small single channel conductance. Thus, for example, a T-type channel exhibits a single channel conductance of from about 4 pS to about 12 pS (e.g., from about 6 pS to about 10 pS), and typically from about 7 pS to about 9 pS in a solution with a  $Ba^{2+}$  concentration of about 0.1 M.

15 The isolated or substantially purified nucleic acid of the present invention encodes all or part of any T-type calcium channel having at least one of the aforementioned electrophysiological properties when properly assembled within a cellular membrane. The general structure of calcium channels is summarized above and is otherwise known in the art. Thus, for example, the nucleic acid can encode one  
20 of the four functional domains mentioned above. As used herein, a domain of a T-type calcium channel is any protein structure able to associate with three other domains to form a tetrameric body functioning as a T-type calcium channel. While the native T-type calcium channel structure includes all four domains in a single polypeptide (indicated in Figures 1A-1E), a domain can exist as a polypeptide species  
25 separate from those containing the other domains. Such separate domains are able to associate within the plasma membrane to form a functional channel. Alternatively, where a plurality of domains are linked within a common polypeptide, the linkage can deviate substantially from the native linkage. Thus, for example, the domains can be linked by polypeptide sequences other than those sequences linking the domains in the  
30 native protein (e.g., non-native polyglutamate linkages). Indeed, the domains themselves can include non-native linkages between membrane-spanning elements within the domains. Aside from these modifications, the nucleic acid can encode a chimeric calcium channel domain (or an entire channel) comprising a portion of a T-type calcium channel and a portion derived from another calcium channel (or other  
35 channel) protein. For example, the chimera can include portions of domains from T-type channels responsible for low voltage gating and portions of domains from other calcium channels responsible for slow inactivation. Such a protein exhibiting T-type gating but longer inactivation kinetics would facilitate pharmacological research.

As mentioned, nucleic acids of the present invention can encode an entire T-type channel (i.e., a T-type channel protein comprising four functional domains). It has been discovered that at least three genes encoding T-type calcium channels exist in humans and rats (i.e.,  $\alpha 1G$  (or  $Ca_vT.1$ ),  $\alpha 1H$  (or  $Ca_vT.2$ ), and  $\alpha 1I$  (or  $Ca_vT.3$ )), and alternate splicing of these isoforms exist. Examples of the amino acid sequences of full-length T-type channels, and the sequences of suitable coding nucleic acids are set forth at SEQ ID NOs:1-8 ( $\alpha 1G$  sequences), SEQ IS NOs:9-10 ( $\alpha 1H$  sequences), and SEQ ID NOs: 11-12 ( $\alpha 1I$  sequences). However, the invention is not limited to these exemplary sequences. Indeed, as mentioned, an amino acid sequence of a T-type calcium channel can vary from those listed, and it is within the state of the art to change a nucleotide sequence encoding a T-type channel to introduce mutations into the protein. Indeed, for conducting electrophysiological assays, it may be desirable to introduce mutations into such a protein. For example, mutations comprising insertions or deletions can be introduced on either the amino- or carboxy-terminus of the protein, or such mutations can be intrasequence insertions or deletions. Where the electrophysiological properties of the calcium channel are to be conserved, such mutations preferably are in regions other than the membrane spanning domains. However, in some applications (e.g., to decrease inactivation kinetics), the changes can be within the membrane-spanning regions. Moreover, as mentioned above, the sequence can form a protein having only one functional domain of a T-type calcium channel. Additionally, the sequence can also form a chimeric protein or domain, such as those described above.

Aside from insertions and deletion mutations of native T-type calcium channel sequences, a T-type calcium channel can include substitutions of amino acid residues, e.g., for those indicated in SEQ ID NOs:1-12. Preferably, and especially where such a substitution is within a membrane spanning region, the substitution is conservative. Thus, within membrane spanning domains, positively-charged residues (H, K, and R) preferably are only substituted with positively-charged residues; negatively-charged residues (D and E) preferably are only substituted with negatively-charged residues; neutral polar residues (C, G, N, Q, S, T, and Y) preferably are only substituted with neutral polar residues; and neutral non-polar residues (A, F, I, L, M, P, V, and W) preferably are only substituted with neutral non-polar residues. Preferably, any amino-acid substitution within the membrane-spanning regions does not alter this conservation. Most preferably, any substitution, deletion, or insertion does not alter the IVS4 domain. In each of the exemplary T-type calcium channel  $\alpha$  subunit sequences, the putative IVS4 region comprises SEQ ID NO:13. Given the strong sequence conservation among families of voltage-gated ion channels, it is likely that this sequence or a derivative sequence, will be present in T-type channels. Thus, the

present invention provides any T-type calcium channel (or a nucleic acid encoding such a T-type calcium channel) comprising SEQ ID NO:13 or a sequence derived from SEQ ID NO:13 having conservative amino acid substitutions, as described above.

5           The nucleic acid of the present invention encoding all or a part of a T-type calcium channel can be isolated via any suitable method. For example, prior to the present invention, one of skill in the art could design a probe based on the sequence of known, non-T-type, calcium channels and use such probe to screen a genetic library. If such a screen were to identify a putative calcium channel, the researcher could then  
10 attempt to clone the entire nucleic acid to characterize it. Similarly, prior to the present invention, to isolate a nucleic acid encoding a T-type calcium channel, one of skill in the art could consult publicly available databases containing DNA sequences (e.g., Genbank) to locate nucleic or amino acid sequences representing a portion of a T-type calcium channel protein or nucleic acid. However, such databases contain no  
15 sequence for a full-length T-type calcium channel or identify any sequence as a T-type channel. Such methods assume that T-type calcium channels share sufficient sequence identity with known calcium channel nucleic acids to cross-hybridize, an assumption not supported by any published report. Moreover, prior to the present invention, no partial sequence in such databases was identified as corresponding to a  
20 T-type calcium channel. Thus, prior to the present invention, the presence of partial sequences in the public DNA databases could facilitate the isolation of T-type calcium channels only with the exercise of a considerable degree of speculation on the part of the researcher.

By providing several sequences pertaining to T-type calcium channels and a  
25 comparison presenting conserved regions and domains, the present invention greatly facilitates the isolation of other nucleic acids encoding T-type calcium channels (or derivatives thereof) with much less experimentation. Thus, while any of the methods discussed above can be employed to isolate other members of this genus, preferably, a nucleic acid encoding a T-type calcium channel is isolated by probing a genetic library  
30 using a probe that hybridizes to a DNA encoding a peptide sequence contained in (or similar to) a known T-type calcium channel (e.g., SEQ ID NOs:1-12). To facilitate the isolation of a T-type calcium channel, the present invention provides an isolated polynucleotide hybridizing to a portion of the nucleic acid of the present invention encoding a T-type calcium channel (or a portion thereof). Thus, for example, the  
35 present invention includes an isolated polynucleotide hybridizing to SEQ ID NO:1-12. The isolated polynucleotide can hybridize to all or any portion of the sequence encoding the T-type calcium channel.

To isolate such a polynucleotide, any portion of a sequence encoding a T-type calcium channel can be employed as a probe to screen a genetic library, and such screening can be accomplished by standard techniques known in the art. While the probe can hybridize to any portion of such a DNA, preferably the probe is designed to hybridize to a DNA encoding a polypeptide sequence that is highly conserved among T-type calcium channels but is less conserved between the genus of T-type calcium channels and other proteins. Such peptide sequences are readily apparent from the sequence comparison set forth in Figures 1A-1E. Generally, the specificity of hybridization in a genetic screen varies depending on the length of the probe and the stringency (e.g., temperature, salt and detergent concentration, etc.) of hybridization. Stringency of hybridization is broadly classified as "high," "moderate," or "low," and the parameters of these terms are well recognized in the art (see, e.g., Sambrook et al., "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Press, 1989). The isolated polynucleotide hybridizing to a portion of the nucleic acid encoding a T-type calcium channel can hybridize under any desired stringency conditions. However, for identifying other T-type channels, preferably, the hybridization occurs under moderate stringency, and most preferably under high stringency.

Of course, the isolated or substantially purified polynucleotide can itself be employed as a probe to screen a library as described to isolate a second nucleic acid. In such a screen, one of the polynucleotides will be complementary to a portion of the sequence encoding the T-type calcium channel, and the other isolated nucleic acid will be "sense." Preferably, one of the two isolated polynucleotides (the "sense" strand) itself encodes a T-type calcium channel, or at least one domain thereof. Such a sequence can be cloned to be operably linked to suitable regulatory elements, as described, to produce a T-type calcium channel. Thus, aside from using the nucleic acid of the present invention to produce a T-type calcium channel, the nucleic acids of the present invention are also useful for isolating other sequences encoding T-type calcium channels, or derivatives thereof.

However isolated, the isolated or substantially purified nucleic acid of the present invention is useful, in part, for producing all or a portion of a T-type calcium channel. Thus, the nucleic acid can be introduced into a suitable milieu for driving its expression. Because T-type channels are transmembrane proteins, preferably such a milieu is a living cell. However, it should be understood that the nucleic acid can also be expressed *in vitro* under conditions, such as those known in the art, suitable for *in vitro* transcription and translation. However produced, the present invention includes any protein, such as a recombinant protein or an isolated or substantially purified protein, including all or a portion of a T-type calcium channel or a protein derived from a T-type calcium channel.

For expression in a living cell, the nucleic acid must be introduced into the cell. As nucleic acids are generally introduced into cells as part of genetic vectors, the present invention provides a vector having a T-type calcium channel nucleic acid of the type described above. Any type of vector suitable for introducing the nucleic acid into a host cell is within the context of the present invention. Examples of such vectors include naked DNA and RNA vectors (such as oligonucleotides, plasmids, capped cRNA, etc.), viral vectors such as adeno-associated viral vectors (Berns et al., *Annals of the New York Academy of Sciences*, 772, 95-104 (1995)), adenoviral vectors (Bain et al., *Gene Therapy*, 1, S68 (1994)), herpesvirus vectors (Fink et al., *Ann. Rev. Neurosci.*, 19, 265-87 (1996)), packaged amplicons (Federoff et al., *Proc. Nat. Acad. Sci. USA*, 89, 1636-40 (1992)), papilloma virus vectors, picornavirus vectors, polyoma virus vectors, retroviral vectors, SV40 viral vectors, vaccinia virus vectors, and other vectors. Once a given type of vector is selected, its genome must be manipulated for use as a background vector, after which it must be engineered to incorporate exogenous polynucleotides. Such manipulations are known in the art.

The vectors of the present invention are useful for introducing a nucleic acid encoding all or a portion of a T-type calcium channel into a host cell. Thus, the present invention provides a cell into which the vector of the present invention has been introduced. The host cell can be any cell suitable for expressing the nucleic acid (e.g., bacteria, insect cells, mammalian cells, etc.). The host cell can thus be *in vitro* or *in vivo*. Preferably the cells do not exhibit native T-type calcium current. A preferred cell type is HEK-293 cells because they contain genetic elements that facilitate the expression of transgenes from a variety of expression vectors. For facilitating electrophysiological recordings, oocytes (e.g., *Xenopus* oocytes) are preferred, as they are large and readily handled.

The vector can be introduced into the cell in any manner suitable for the cell type and vector employed. In one embodiment, the vector can be used to prepare an RNA transcript *in vitro* (e.g., a capped cRNA) which is then introduced into the host cell by standard methods (such as injection). Such techniques are preferred when the host cells do not actively transcribe DNA (such as oocytes). In other embodiments, a DNA vector is introduced into the cell such that it is transcribed within the cell. For example, the vector can be introduced into the cell such that it forms an extrachromosomal segment of genetic material in the cell, as is the case with many types of viral vectors. Alternatively, the vector can introduce the nucleic acid into the chromosomal DNA of the host cell.

Preferably, a cell into which the nucleic acid is introduced is also able to express the nucleic acid to produce the  $\alpha$  subunit protein. The expression of the nucleic acid can be detected by probing the cell for the presence of T-type calcium

channel mRNA, such as via Northern hybridization analysis, in situ hybridization, etc. More preferably, however, the cell is able to express the nucleic acid to produce the protein including all or a portion of a T-type calcium channel. In such cells, expression of the nucleic acid is confirmed by detecting the protein, for example, by  
5 probing cellular extracts with an antibody recognizing the protein (e.g., on a Western blot, etc.).

In the membrane of the cell producing the protein, the expressed protein contributes to the formation of a functional calcium channel. Where the protein encodes an entire  $\alpha$  subunit, the full protein will possess some or all of the  
10 electrophysiological properties of T-type calcium channels described above. Where the protein encodes less than an entire channel  $\alpha$  subunit (e.g., a domain), the protein will aggregate with other constituent domains in the membrane to form a functional channel. Thus, the presence of the protein can be detected by assaying the cell for T-type calcium channel activity. Indeed, assaying for channel activity serves to  
15 determine whether a nucleic acid encoding a putative calcium channel, in fact, encodes a species of T-type channel (as opposed to a member of another genus of calcium channels). For example, when large cells (e.g., oocytes) are used as the host cells, the electrophysiological properties of the channel can be investigated. Thus, the membrane activity of whole cells expressing the nucleic acid can be measured  
20 directly, such as via patch clamp techniques using a voltage clamp electrode and a current electrode (Bernal et al., *J. Pharmacol. Exp. Ther.*, 282, 172-80 (1997)). Alternatively, the activity of single channels can be measured, such as with a standard depolarizing bath and pipette solutions (Lacerda et al., *Biophys. J.*, 66, 183-43 (1994)). However measured, the properties of cells into which the putative nucleic  
25 acid is introduced are compared to the channel conductance, voltage dependency, activation kinetics, inactivation kinetics, or tail current known for T-type channels and discussed above. A measure of current density (e.g., pA/pF) can also be used to assess the level of gene expression in the cells, normalizing for cellular volume.

While, in accordance with the present invention, an isolated cell into which the  
30 T-type calcium channel nucleic acid has been introduced (and preferably stably expressing the nucleic acid to produce the protein) can be prepared, preferably, such transfection protocols result in a population consisting essentially of such transfected cells. For standardizing the results of many experiments, it is even more desirable to employ an established cell line consisting essentially of such cells. Preferably, for use  
35 in high throughput assays, cell lines stably expressing a T-type calcium channel exhibit a current density of at least about 40 pA/pF (e.g., at least about 45 pA/pF), such as about 50 pA/pF or even 55 pA/pF or higher. Preferably, a cell line in accordance with the present invention is able to propagate the nucleic acid through

several passages (e.g., for at least 10 passages), and, preferably, the nucleic acid is stably integrated into the chromosomes of such cells. Thus, the cell line can propagate the nucleic acid for at least 20 passages, and more preferably significantly more than 20 passages (e.g., at least about 25 passages, or even more).

5           Regardless of the cell system, the ability to express a T-type calcium channel nucleic acid within host cells to produce an active channel permits the channel to be further studied. In this regard, the present invention provides a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel, as herein described.

10       The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter, the presence or absence of calcium flux in response to a change in membrane potential is assayed. Any such assay can be employed within the context of the present invention, (e.g., using labile dyes, radioisotopes (e.g.,  $^{45}\text{Ca}$ ), recording electrophysiological changes in the membrane,  
15       etc.). A quick method of assaying for calcium flux is first to introduce a calcium-sensitive labile dye into the cells. For example, the dye can be one such as those that fluoresce or change color in the presence of calcium, many of which are known to those of skill in the art (e.g., Indo-1). Thereafter, the cells are exposed to a depolarizing solution containing high (e.g., about 50 mM) potassium concentration  
20       and a drug, and the reaction of the labile dye is compared to control cells. Using a labile dye affords the ability to assay many putative drugs quickly in a high throughput assay for putative drugs affecting T-type channels. For example, the initial screening can be carried out in 96 well plates. Moreover, dose-response data can be readily generated by exposing the cells to several concentrations of the same putative  
25       drug.

          Once a putative drug is detected, its effect on the electrophysiology of the cell (e.g., single channel conductance, voltage dependency, activation kinetics, inactivation kinetics, and tail current of the cells) can be investigated in detail.

30       Generally, the effect of the putative drug on T-type calcium currents is assessed by measuring the various electrophysiological parameters in the presence of various concentrations of the drugs and comparing the data to untreated (or sham-treated) control cells. Cells preferably are maintained in a continuous perfusion chamber during such experiments to facilitate changing solutions. The inventive method of identifying a drug which affects T-type calcium channels can employ any nucleic acid  
35       encoding a T-type calcium channel (or derivative thereof), such as those nucleic acids described herein. In fact, as several isoforms of T-type channel exist, the assay method can be repeated using nucleic acids encoding different isoforms to identify

drugs that preferentially target a given isoform, or drugs which affect more than one isoform of T-type calcium channels.

Aside from affording an *in vitro* assay for detecting potential therapeutic or investigative drugs targeting T-type calcium channels, the method of expressing the T-type calcium channel nucleic acid can also be used *in vivo*. For example, as mentioned, several neurological and muscular diseases or disorders have implicated mutations affecting native nucleic acids encoding T-type calcium channels. The present invention, thus, provides a method of treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid. The method involves introducing a vector having the T-type calcium channel nucleic acid into cells of a host in which native expression of the nucleic acid is deficient. Thus, for example, for treating cardiomyopathy associated with deficiencies in T-type calcium channels, the vector is introduced into myocardial cells. Similarly, for treating forms of epilepsy associated with deficiencies in T-type calcium channels, the vector is introduced into neurons (e.g., thalamic neurons). Within the target cells, the nucleic acid within the vector is expressed to produce active T-type calcium channel. By similar methods, an nucleic acid having a sequence antisense to a sequence encoding a T-type calcium channel (or a portion thereof) can be expressed within a cell. The presence of an antisense sequence can down-regulate the expression of native T-type calcium channel genes by hybridizing to T-type channel mRNA within the cell. Thus, the present invention is useful to treating disorders associated with over-expression of T-type calcium channels.

T-type channel proteins (such as whole T-type calcium channels, domains of such channels, chimeras including portions of T-type calcium channels, etc.) can be employed to generate antibodies (e.g., immunoglobulins) to T-type calcium channels. Thus, the present invention provides an isolated and substantially purified antibody molecule recognizing an epitope on a T-type calcium channel. Such antibodies can be monoclonal antibodies or polyclonal antisera. Antibodies recognizing T-type calcium channels can be used to purify the channels from cell extracts or other solutions by standard methodologies (e.g., immunoprecipitation). Moreover, depending on the location of the epitopes for the antibodies on the T-type calcium channel, the antibodies can be used to affect the channel proteins present on the surface of cells. Thus, antibodies directed to T-type calcium channels are potential reagents for studying the channels as well as for therapy.

Such antibodies can be produced by any suitable method, many of which are well known in the art. Thus, for example, the antibodies can comprise polyclonal antisera obtained from inoculated animals. Alternatively, the antibody molecules can be monoclonal antibodies obtained from a cell line (e.g., a hybridoma cell line). Thus,



the present invention provides a cell which produces such antibodies. Such a cell can be *in vitro* or *in vivo*; however, where the cell is *in vitro*, preferably it is within an established cell line consisting essentially of such cells.

Several examples are presented below to illustrate the invention. Taken  
5 together, the examples demonstrate the cloning of twelve novel proteins and their characterization as T-type calcium channel  $\alpha$  subunits. These examples are included here for purely illustrative purposes; as such, they are not to be construed so as to limit the scope of any aspect of the invention.

Many procedures employed in the following examples are techniques routinely  
10 performed by one of ordinary skill in the art (see generally Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)) and are not discussed in detail. However, some reagents and methods deserve specific description. Thus, for example, *in vitro* translation and expression were conducted as described previously (Schneider et al., *Receptors and Channels*, 2,  
15 255-70 (1995)). *Xenopus laevis* oocytes were prepared as described previously (Bernal et al., *J. Pharmacol. Exp. Ther.*, 282, 172-80 (1997)). To express proteins, 10 or 30 ng of capped cRNA was injected into the oocytes in a volume of 50 nl. For single channel recording, oocytes were injected with 100 ng capped cRNA and incubated for one week prior to assay.

20 Cells were voltage clamped using a two-microelectrode voltage clamp amplifier as described (Bernal et al., *J. Pharmacol. Exp. Ther.*, 282, 172-80 (1997)). The standard bath solution contained the following: 40 mM Ba(OH)<sub>2</sub>, 50 mM NaOH, 1 mM KOH, 0.1 mM EDTA, and 5 mM HEPES, adjusted to pH 7.4 with methanesulfonate. The osmolality of the 2 mM Ba<sup>2+</sup> and 10 mM Ba<sup>2+</sup> solutions was  
25 balanced by increasing the NaOH concentration as described (Lory et al., *J. Physiol. (London)*, 429, 95-112 (1990)). Voltage and current electrodes (1.5-1.8 M tip resistance) were filled with 3 M KCl. Except as noted, data were acquired at 4 kHz using the pCLAMP system, and filtered at 1 kHz. Data were analyzed using pCLAMP software. Boltzman fits and linear regression were calculated using Prism.

### 30 EXAMPLE 1

This example demonstrates the cloning and characterization of putative T-type calcium channels.

A search of the Genbank library was conducted to identify clones identified as  
35 having some degree of homology to known calcium channel sequences. The search identified an expressed sequence tagged (EST) partial sequence in a human brain clone (H06096), which was used as a probe to screen a  $\lambda$ gt10 cDNA library prepared

from rat brain. Successive screening of the cDNA library identified five overlapping clones which were aligned to construct an entire cDNA sequence, termed  $\alpha 1G$ .

The  $\alpha 1G$  cDNA was cloned into the pSP72<sup>TM</sup> vector and sequenced by standard computer-assisted sequencing. Using the  $\alpha 1G$  cDNA, the amino acid  
5 sequence of the  $\alpha 1G$  protein was deduced and compared to the sequences of other known calcium channel  $\alpha$  subunits. By similar methods, homologous human (H19230 and R19524) and mouse (AA286626) EST clones were also identified and partially sequenced, and alternately spliced variants were identified. The deduced  
10 cDNA and amino acid sequences for eight full-length  $\alpha 1G$  T-type channels are set forth, respectively, as SEQ ID NOs:1-8.

A second T-type calcium channel, termed  $\alpha 1H$ , was isolated by screening a human heart cDNA library with a fragment of the  $\alpha 1G$  sequence. An alternately spliced isoform was also identified. The full-length cDNA and amino acid sequences for these  $\alpha 1H$  T-type channels are set forth, respectively, as SEQ ID NOs:9 and 10.

15 A third T-type calcium channel, termed  $\alpha 1I$ , was isolated by screening a rat brain cDNA library at low stringency using a fragment of the rat  $\alpha 1G$  gene. Fifty plaques were identified, many of which were not detected in a second screening. A third screening with a fragment from  $\alpha 1H$  identified two clones. Subsequent screening, and the use of the GenBank database, led to the identification of the full  
20 length rat and human cDNA and amino acid sequences, set forth at SEQ ID NOs: 11 and 12, respectively.

The  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  amino acid sequences were compared to each other and a known calcium channel ( $\alpha 1E$ ) to investigate the conservation of protein  
25 acid sequences within the putative membrane-spanning domains are about 90 % identical to each other, while the  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  sequences are only roughly 40 % identical to the  $\alpha 1E$  clone.

Figures 1A-1E indicate this conservation between the proteins. The conservation of charged residues, particularly in the S4 domains, is consistent with the  
30 role of the  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  proteins as ion channels. However, two of the glutamates associated with ion specificity in other calcium channels have been replaced with aspartate, suggesting altered ion selectivity. Strikingly,  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  display only low homology to sequences linking the membrane-spanning regions within each domain, and even less homology between the intracellular loops linking  
35 domains. Notably, neither  $\alpha 1G$ ,  $\alpha 1H$ , nor  $\alpha 1I$  possesses sequences known to bind  $\beta$  subunits or  $Ca^{2+}$  ions.

## EXAMPLE 2

This example demonstrates the production of cell lines stably expressing the cloned  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  proteins.

HEK-293 cells were transfected with either the rat  $\alpha 1G$  cDNA (SEQ ID NO:1), the human  $\alpha 1H$  cDNA (SEQ ID NO:9), or the rat  $\alpha 1I$  cDNA (SEQ ID NO:11). As a control, cells were also transfected with human  $\alpha 1E$  plus human  $\beta 3$  (Schneider et al., *Receptors Channels*, 2, 255-70 (1994); Murakami et al., *Eur. J. Biochem.*, 236, 138-43 (1996)). The DNA constructs included a neomycin resistance gene conferring resistance to G418. The cells were cultured under standard conditions using medium containing G418 to select for stable transformants.

Surviving clones were expanded and assayed for electrophysiological activity to determine the presence of channels within the membrane. Whole-cell currents were recorded from ruptured patches using an Axopatch 200A amplifier, Digidata 1200 A/D converter, and pCLAMP 6.0 software. Data were digitized at 2 kHz and filtered at 1 kHz or off-line. All experiments were performed at room temperature. Pipettes were made out of TW-150-6 capillary tubing (World Precision Instruments, Inc., Sarasota, FL), using a Model P-97 Flaming-Brown pipette puller (Sutter Instrument Co., Novato, CA). The internal pipette solution contained the following: 55 mM CsCl, 75 mM CsSO<sub>4</sub>, 10 mM MgCl<sub>2</sub>, 0.1 mM EGTA, 10 mM HEPES, pH adjusted to 7.2 with CsOH. The external Tyrodes solution was the following: 140 mM NaCl, 6 mM KCl, 2 mM CaCl<sub>2</sub>, 10 mM glucose, 5 mM HEPES, pH 7.4. The recording solution contained the following: 10 mM BaCl<sub>2</sub> solution (or 2 mM CaCl<sub>2</sub>), 140 mM tetraethylammonium (TEA) chloride, 5 mM CsCl, 1 mM MgCl<sub>2</sub>, 5 mM glucose, and 10 mM HEPES, pH adjusted to 7.4 with TEA-OH. Under these solution conditions the pipette resistance was typically 1.5-2.5 M $\Omega$ . Cell capacitance was measured by integrating the charging current during a 10 mV hyperpolarizing pulse (holding potential -80 mV).

Using these recording techniques, values for pA/pF were obtained for each cell line, which is a measure of current density normalizing for cell size. One clone (#N2) expressed the rat  $\alpha 1G$  protein and has a current density of 42 pA/pF. Another clone (#13), expressed the human  $\alpha 1H$  protein and exhibited a current density of 53 pA/pF. Three clones (#11, #19, and #25) expressed the rat  $\alpha 1I$  protein and exhibited current densities of 40 pA/pF, 45 pA/pF, and 55 pA/pF, respectively.

## EXAMPLE 3

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type current-voltage relationships.

Current traces were elicited by depolarizing voltage clamp pulses of the membranes of cells. The  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  proteins were produced in *Xenopus laevis* oocytes by linearizing the DNA vectors containing the coding sequences, and transcribing the coding sequences *in vitro* by standard methods. Oocytes were then injected with the capped RNA.

Figures 2A-2E depict data obtained from these experiments using cells injected with  $\alpha 1G$  (Figure 2A),  $\alpha 1H$  (Figure 2B), and  $\alpha 1I$  (Figure 2C) and  $\alpha 1E$  (Figure 2D). These data indicate that cells expressing  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  exhibit T-type calcium current, while oocytes expressing  $\alpha 1E$  as well as uninjected oocytes (Figure 6A) do not.

Current voltage curves were developed using cells injected with  $\alpha 1G$ ,  $\alpha 1H$ ,  $\alpha 1I$ , and  $\alpha 1E$ . Figures 3A depicts such data generated in a 10 mM  $Ba^{2+}$  test solution. These data were transformed into conductance and fit with a Boltzman equation to determine the midpoint of activation ( $V_{0.5}$ ). Gating potentials for  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  ( $-38 \pm 1$  mV  $n=8$ ,  $-44$  mV  $\pm 1$  mV,  $n=10$ , and  $-31$  mV  $\pm 1$  mV,  $n=6$ , respectively) were in accordance with the gating potential measured for the HEK-293 cells ( $-41 \pm 1$  mV,  $n=10$ ), while  $\alpha 1E$  required significantly more positive potentials to open ( $-2.6$  mV  $\pm .4$  mV,  $n=3$ ).

To compare the characteristics with published values (Huguenard, *Ann. Rev. Physiol.*, 58, 329-48 (1996)), the  $\alpha 1G$  current was recorded at varying concentrations of  $Ba^{2+}$ . As indicated in Figure 3B, in solutions containing 2 mM  $Ba^{2+}$ ,  $V_{0.5}$  was  $-46.5$  mV, and the slope factor ( $k$ ) was 6.6 ( $n=7$ ). However, when the  $Ba^{2+}$  concentration was 40 mM,  $V_{0.5}$  was recorded at  $-21$  mV, presumably due to the results of barium on surface charge screening (see, e.g., Wilson et al., *J. Membrane Biol.*, 72, 117-30 (1983)). Similar values were recorded for  $\alpha 1H$  and  $\alpha 1I$ .

These results indicate that  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  are low-voltage activated calcium channels (i.e., from about  $-60$  mV to about  $-30$  mV in 10 mM  $Ba^{2+}$ ).

#### EXAMPLE 4

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type tail current.

Tail current was measured at  $-90$  mV after first opening the channels with a voltage step to  $-10$  mV. The voltage-dependence of tail current in cells expressing  $\alpha 1G$  (oocytes)  $\alpha 1H$  (HEK 293 cells), and  $\alpha 1I$  (HEK 293 cells) was measured at varying test potentials. As a control, tail current was also measured from a high voltage activated channel  $\alpha 1E$ , which Raw data from recordings data were fit with a single exponential and plotted as a function of depolarization potential (Figure 4).

These results demonstrate that the tail currents for the cloned  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  calcium channels are voltage-dependent, consistent with known T-type calcium tail currents. Additionally, these data demonstrate that the tail current for each of the cloned channels is between about 1 ms and about 10 ms following repolarization to a membrane potential from about  $-80$  mV to about  $-60$  mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

#### EXAMPLE 5

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type single channel conductance.

Measurement of single channel conductance is complicated by the low probability of channel opening at negative potentials when the driving force is large. Thus, single channel conductance was measured similarly for measurements of tail currents to enhance channel opening at negative potentials. Single channels were measured with standard depolarizing bath and pipette (115 mM  $\text{BaCl}_2$ , 1 mM EGTA, and 10 mM HEPES, pH 7.4) solutions (Lacerda et al., *Biophys. J.*, 66, 1833-43 (1994)). Data were analyzed with TRANSIT (VanDongan, *Biophys J.*, 70, 1303-15 (1996)). Single channel amplitudes were measured by averaging the values obtained from Gaussian fits to all-points histograms of traces with openings, selected openings, or amplitude histograms of idealized openings. It has been reported that some oocytes contain a native 9 pS channel. These endogenous channels can be distinguished by their 2-fold larger current amplitudes at the potentials tested (e.g.,  $-20$  mV,  $i = 0.8$  for endogenous channels as opposed to 0.4 pA for  $\alpha 1G$ ). However, such endogenous channels were not detected either at the whole cell or single channel level in the oocytes tested.

Current through the main open state of each open channel was measured at each potential and plotted against each test potential. Single channel currents for several patches were then averaged and plotted as a function of test potential, wherein the slope of the plot indicated the single channel conductance. The average slope conductance of the  $\alpha 1G$  channel was measured at  $7.5 \pm 1.5$  pS, which corresponds with the reported values for T-type calcium channels (Hugenard, *Ann. Rev. Physiol.*, 58, 329-48 (1996)). Similar results were also obtained with both  $\alpha 1H$  ( $10.8 \pm 1.4$  pS). Data collected from recordings of the  $\alpha 1I$  channels indicate that they open to two distinct amplitudes. The conductance for the small amplitude  $\alpha 1I$  openings was measured at  $3.9 \pm 0.5$  pS, while that for the large  $\alpha 1I$  openings was measured at  $11.4 \pm 0.5$  pS).

These results indicate that the cloned  $\alpha 1G$ ,  $\alpha 1H$ , and  $\alpha 1I$  proteins exhibit T-type single-channel conductance (e.g., from about 4 to about 12 pS).

## EXAMPLE 6

This example demonstrates that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels.

5 HEK-293 cells were subjected to treatment as indicated above in Example 3, except that an experimental group of cells were exposed to a solution containing 1  $\mu$ M mibefradil, a known inhibitor of T-type calcium current. As depicted in Figure 5A, the presence of mibefradil almost completely abolished T-type current in cells  
10 expressing  $\alpha 1G$ . Cells expressing either  $\alpha 1G$  or  $\alpha 1H$  were similarly treated using various concentrations of mibefradil to determine a dose-response relationship. These results, depicted in Figure 5B, demonstrate that about 50% inhibition was achieved at a mibefradil concentration of 1  $\mu$ M.

15 All of the references cited herein, including patents, patent applications, and publications, are hereby incorporated in their entireties by reference.

While this invention has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations of the preferred embodiments may be used and that it is intended that the invention may be practiced otherwise than as specifically described herein. Accordingly, this  
20 invention includes all modifications encompassed within the spirit and scope of the invention as defined by the following claims.

What is claimed is:

1. A isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel  $\alpha$  subunit.

5 2. The nucleic acid of claim 1, wherein said protein comprises an entire T-type calcium channel  $\alpha$  subunit.

3. The nucleic acid of claim 2, wherein said protein comprises SEQ ID NO:13.

10 4. The nucleic acid of any of claims 1-3, wherein said calcium channel begins to gate from about -60 mV to about -30 mV in 2 mM  $Ba^{2+}$ .

5. The nucleic acid of any of claims 1-4, wherein said calcium channel exhibits a tail current of from about 1 ms to about 10 ms following repolarization to a membrane potential from about -80 mV to about -60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

15 6. The nucleic acid of any of claims 1-5, wherein said calcium channel exhibits a single channel conductance of from about 4 pS to about 11 pS in a solution with a barium ion concentration of about 100 mM.

7. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of any of claims 1-6.

20 8. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of claim 7.

9. The nucleic acid of claim 8 comprising a sequence encoding at least one domain of a T-type calcium channel  $\alpha$  subunit.

10. A vector comprising the nucleic acid of any of claims 1-9.

25 11. A cell into which the vector of claim 10 has been introduced.

12. The cell of claim 11, which expresses said nucleic acid to produce said protein.

13. The cell of claim 11 or 12, which stably expresses said nucleic acid to produce said protein.

30 14. A population of cells consisting essentially of cells according to any of claims 11-13.

15. An established cell line consisting essentially of cells according to any of claims 11-13.

35 16. A method of identifying a drug which affects T-type calcium channels, said method comprising expressing a T-type calcium channel in a cell, exposing said cell to a putative drug, and measuring the calcium flux through the membrane of said cell in response to a change in membrane potential.

17. The method of claim 16, wherein said calcium flux is assayed by using a calcium-sensitive labile dye within said cell.

18. The method of claim 16, wherein said calcium flux is assayed by measuring the electrophysiological properties of said cell.

5 19. The method of claim 16, wherein said calcium channel comprises SEQ ID NO:13.

20. An isolated or substantially purified immunoglobulin recognizing an epitope on a T-type calcium channel protein.

21. A cell *in vitro* which produces the immunoglobulin of claim 20.

10 22. An established cell line consisting essentially of cells according to claim 21.



hCavT1a MDEEDGAGAEESGQPR-----SFMRLDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVFFVLSQDSRPSWCLRTVCNPW  
 rCavT1a MDEEDGAGAEESGQPR-----SFTQNDLSGAGRQPGPGSTEKDPGSADSEAEGLPYPALAPVFFVLSQDSRPSWCLRTVCNPW  
 hCavT2a MTEGARAADDEVVRVPLGRRPWCVGVGPGEPGRGAGTRGGGFGELGVSPSESPAARCAELGADEEQRPYPALAAATVFFCLGQTRPRSWCLRLVCNPW  
 hCavT3 MAESASPPSSAAA-----PAAEPGVTTTEQPGPRSPSPSPGLEEPLDGADPHVPHDLAPIAFFCLRQTTSRPNWCIKMVCNPW  
 rCavT3 MADSNLPPSSAAAP-----APEPG--ITEQPGPRSPSPSPSPGLEEPLDGNPDVPHPDLPAPVAFCLRQTTSRPNWCIKMVCNPW

## IS3

hCavT1a FERISMLVILLNCVTLGMRPCEDIACDQRCRILQAFDDFIFAFFAVEMVVKWALGIFGKKCYLGD<sup>IS2</sup>TWNRDFFIVIA<sup>IS1</sup>AGMLEYSLDLQNV<sup>IS3</sup>SFAVRTV  
 rCavT1a FERVSMVLVILLNCVTLGMRPCEDIACDQRCRILQAFDDFIFAFFAVEMVVKWALGIFGKKCYLGD<sup>IS2</sup>TWNRDFFIVIA<sup>IS1</sup>AGMLEYSLDLQNV<sup>IS3</sup>SFAVRTV  
 hCavT2a FEHVSMLVIMLNCVTLGMRPCEDVECGSERCNILEAFDAFIFAFFAVEMVVKWALGIFGKKCYLGD<sup>IS2</sup>TWNRDFFIVIA<sup>IS1</sup>AGMLEYSLDGHNV<sup>IS3</sup>LSAIRT  
 hCavT3 FECVSMVLVILLNCVTLGMYQPCDDMDCLSDRCKIMQVDDFIFIFAMEMVLKMWALGIFGKKCYLGD<sup>IS2</sup>TWNRDFFIVIA<sup>IS1</sup>AGMLEYSLDLQIN<sup>IS3</sup>LSAIRT  
 rCavT3 FECVSMVLVILLNCVTLGMYQPCDDMDCLSDRCKILQVDDFIFIFAMEMVLKMWALGIFGKKCYLGD<sup>IS2</sup>TWNRDFFIVIA<sup>IS1</sup>AGMLEYSLDLQIN<sup>IS3</sup>LSAIRT

## IS5

hCavT1a RVLRLPLRAINRVPSMRILVTL<sup>IS4</sup>LLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTE<sup>IS5</sup>NEDESPFICSQPRENGMRS  
 rCavT1a RVLRLPLRAINRVPSMRILVTL<sup>IS4</sup>LLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LEPYQTE<sup>IS5</sup>NEDESPFICSQPRENGMRS  
 hCavT2a RVLRLPLRAINRVPSMRILVTL<sup>IS4</sup>LLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDFAVRNNNLTLRPPYQTE<sup>IS5</sup>EEGENPFICSSRRDNGMQK  
 hCavT3 RVLRLPLKAINRVPSMRILVNL<sup>IS4</sup>LLDTPMLGNVLLLCFFVFFIFGIIIGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYQPE<sup>IS5</sup>DEMPFICSLSGDNGIMG  
 rCavT3 RVLRLPLKAINRVPSMRILVNL<sup>IS4</sup>LLDTPMLGNVLLLCFFVFFIFGIIIGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYQPE<sup>IS5</sup>DEMPFICSLTGDNGIMG

## IP LOOP

hCavT1a CRSVPTL<sup>IS6</sup>RGD-----GGPPCGLDYEAYNSSNTTCVNNQY<sup>IS7</sup>TNCSAGEHNPFKGA<sup>IS8</sup>INF<sup>IS9</sup>DNIGYAWIA<sup>IS10</sup>IFQVITLEGWVDIMYFVMDAHSFYNFYFI  
 rCavT1a CRSVPTL<sup>IS6</sup>RGEG-----GGPPCSLDYETYNSSNTTCVNNQY<sup>IS7</sup>TNCSAGEHNPFKGA<sup>IS8</sup>INF<sup>IS9</sup>DNIGYAWIA<sup>IS10</sup>IFQVITLEGWVDIMYFVMDAHSFYNFYFI  
 hCavT2a CSHIPGRDVRMPCTLGWEA-YTQPQAE<sup>IS11</sup>GVGAARNACIN<sup>IS12</sup>WQY<sup>IS13</sup>NVCRSGDSNPHNGA<sup>IS14</sup>INF<sup>IS15</sup>DNICYAWIA<sup>IS16</sup>IFQVITLEGWVDIMYFVMDAHSFYNFYFI  
 hCavT3 CHEIPPLKEQGRECCLSKDDVYDFGAGRODLN<sup>IS17</sup>ASGLCVNWR<sup>IS18</sup>Y<sup>IS19</sup>NVCR<sup>IS20</sup>TGSANPHKGA<sup>IS21</sup>INF<sup>IS22</sup>DNICYAWIVIFQVITLEGWVEIMYFVMDAHSFYNFYFI  
 rCavT3 CHEIPPLKEQGRECCLSKDDVYDFGAGRODLN<sup>IS17</sup>ASGLCVNWR<sup>IS18</sup>Y<sup>IS19</sup>NVCR<sup>IS20</sup>TGSANPHKGA<sup>IS21</sup>INF<sup>IS22</sup>DNICYAGIVIFQVITLEGWVEIMYFVMDAHSFYNFYFI

## IS6

hCavT1a LLIIVGSFFMINCLVVIATQFSETKQRESQ<sup>IS6</sup>LMREQVRFLSNASTLASFSEPGSCYEEL<sup>IS7</sup>LKVLVYILRKAARLAQVSRAAGVVRVGLLSSPAPLGQET  
 rCavT1a LLIIVGSFFMINCLVVIATQFSETKQRESQ<sup>IS6</sup>LMREQVRFLSNASTLASFSEPGSCYEEL<sup>IS7</sup>LKVLVYILRKAARLAQVSRAIGVRAGLLSSPVARSGQEP  
 hCavT2a LLIIVGSFFMINCLVVIATQFSETKQRESQ<sup>IS6</sup>LMREQVRFLSNASTLASFSEPGSCYEEL<sup>IS7</sup>LKVLVYILRKAARLAQVSRAIGVRAGLLSSPVARSGQEP  
 hCavT3 LLIIVGSFFMINCLVVIATQFSETKQREHRLM<sup>IS8</sup>LEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAARLAQVSRAIGVRAGLLSSPVARSGQEP  
 rCavT3 LLIIVGSFFMINCLVVIATQFSETKQREHRLM<sup>IS8</sup>LEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAARLAQVSRAIGVRAGLLSSPVARSGQEP

Fig. 1A

2/10

```

hCavT1a QPSSSCSRSHRRLSVHHLVHHHHHHHHYHGLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSAGPPGGA-----ESVHSFYHADCHLEPVRC
rCavT1a QPSGSCTRSHRRLSVHHLVHHHHHHHHHHYHGLNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPSPGPPRGA-----ESVHSFYHADCHLEPVRC
hCavT2a GHRQRAGRHTASVHHLVYHHHHHHHHHHYHFSHGSPRRPGPEPGACDTRLVRAGAPSPSPGRGPPDAESVHSIYHADCHIEGPQERARVGTCSRSHCRC
hCavT3 -----
rCavT3 -----

hCavT1a QAPPPRSPSEASGRTVGSGKVYPTVHTSPPPPETLKEKALVEVAASSGPPTLTSLN-IPGPPYSSMHKLLLEQTSTGACQSSCKISSPCLKADSGACGPDSC
rCavT1a QAPPPRCPSEASGRTVGSGKVYPTVHTSPPPPEILKOKALVEVAPSPGPPTLTSEN-IPGPPFSSMHKLLLEQTSTGACHSSCKISSPCSKADSGACGPDSC
hCavT2a QPQAGHRAGHHELPHDPALRGGRQQRQHQPRTQCEVGRWTARHRGHGPLSINSPDPYEKIPHVAGEHGLQAPGHLGSLSVPCPLSPPPAGTTLTCELKSC
hCavT3 -----ALGPEAPAPAKPGPHAKEPRHYQLCPQHSPLDPTHTLVQPIPATLASDPASC
rCavT3 -----AMGPGTPAPAKPGPHAKEPSHCKLCPRHSPLDPTHTLVQPIPAISAILASDPSSC

hCavT1a PYCARA-GAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHS-----RR-QRSLGPDAEPSSVLAFWRLICDTFRKIIVDSKYFGRGIM
rCavT1a PYCART-GAGEPESADHVMPDSDSEAVYFTQDAQHSDLRDPHS-----RRQRSLGPDAEPSSVLAFWRLICDTFRKIIVDSKYFGRGIM
hCavT2a PYCTRALEDPEGELSGSESGSDGRGVYFTQDVRHGRWDTPRPRAATDPGPGSPQRRQQRAAPGEPGMGRMLWVTFSGKLRRIVDSKYFSRGIM
hCavT3 PCCQHEGRRPGLGSTDGQEGS-----GSGSSAGGEDEADGDCARSEDGASSELGKEEEEEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIM
rCavT3 PHCQHEAGRPPGLGSTDGQEGS-----GSGGSA--EAEANGDGLQSSDGVSSDLGKEEQE---DGAARLCGDVWRETRKLRGIVDSKYFNRGIM

hCavT1a IAILVNTLSMGIEYHEQPEELTNALIEISNIVETSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPA
rCavT1a IAILVNTLSMGIEYHEQPEELTNALIEISNIVETSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPA
hCavT2a MAILVNTLSMGVEXHEQPEELTNALIEISNIVETSMFALEMLLKLACGGLGYIRNPYNIFDGIIVISVWEIVGQADGGLSVLRTFRLMRVLKVRFLPA
hCavT3 MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMLKLAAFGLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLMRVLKVRFLPA
rCavT3 MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMLKLAAFGLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLMRVLKVRFLPA

hCavT1a LQRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERD-GDTLPDRKNFDSLMLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMT
rCavT1a LQRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERD-GDTLPDRKNFDSLMLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMT
hCavT2a LRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERD-GDTLPDRKNFDSLMLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMT
hCavT3 LRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERD-GDTLPDRKNFDSLMLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMT
rCavT3 LRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERD-GDTLPDRKNFDSLMLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMT

```

Fig. 1B

## IIIS6

hCavT1a FGNVYLFNLLVAILVEGFQAECDANKSEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLPPL-----I IHTAATPMSLPKSTSTGLGEALGPASR  
rCavT1a FGNVYLFNLLVAILVEGFQAECDANKSEPDFFSPSLDGDGDRKKCLALVSLGEHAEELRKSLLPPL-----I IHTAATPMSHPKSSSTGVGEALGSGSR  
hCavT2a FGNVYLFNLLVAILVEGFQAECDANRSDTDEKTSVHFEEDFKLRELQTELKMCSLAVTPNGTWDEAACPLPSSCAQLPRPCLPPRAHHSWMQPPAS  
hCavT3 FGNVYLFNLLVAILVEGFQAECDANRSDSDQSSNIEEFKLEGLDSSGDPKLCPIPMTPNGHLDPPLGCHLGPAGAAGPAPRLSLQPDPMVAL  
rCavT3 FGNVYLFNLLVAILVEGFQAECDANRSDSDQSSNIEEFKLEGLDSDRLKLCPIPMTPNGHLDPPLGCHLGPAGTGTAPRLSLQPDPMVAL

hCavT1a RTSSSGSAEPGAAH-EMKSPPSARSSPHSPWSAASWTSSRSNSLGRAPSLKRR-----SPSGERRSLLSGEGQESQDEEESSEERASP  
rCavT1a RTSSSGSAEPGAAHMKPPSARSSPHSPWSAASWTSSRSNSLGRAPSLKRR-----SPSGERRSLLSGEGQESQDEEESSEEDRASR  
hCavT2a QTLGVAAAAPGTRHWETRSRQPPKFSCLPLGPSGAWSSRRSSWSLGRAQQA-----PACQGERESLLSGEGKSTDDAEEDGRARS  
hCavT3 GSRKSSVMSLGRMSYDQRLSSSSRSYSGPWRSAWASRRSSWSNLKHKPPSAEHESSLAEERGGG-ARVEVAADEGPPRAAPLHTPHAHVHHGPHL  
rCavT3 DSRKSSVMSLGRMSYDQRLSSSSRSYSGPWRSGTWAARRSSWSNLKHKPPSAEHESSLGEGGSCVRACEGAREEAPTRTAPLHAPHAHVHHGPHL

hCavT1a AGSDHRRHRSLEAKSSFDLPDTLQVPGHLRTASGRGSAEH--QDCNGKSAAGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACCLERD  
rCavT1a AGSDHRRHRSLEAKSSFDLPDTLQVPGHLRTASGRGSAEH--QDCNGKSAAGRLARALRTDDPQLDGDADDDEGNLSKGERIQAWVRSRLPACCLERD  
hCavT2a GPRATPLRAESLDPR-----PLRRPPAYQVDRDQGVVALPSDFFLRIDSHREDAEALDDSDSCCLRLHKVLVYPYKQRCRSRRPG  
hCavT3 AHRHRHRRRTSLDNRDSVDLAELVPAVGAHPRAAAGPAGHEDCNGRMPISIAKVETKMGDRGDEDEEIDYTLCFRVRKMDIVYKPDWCEVRE  
rCavT3 AHRHRHRRRTSLDNRDSVDLGELVPVVGASRAAARGAGQAPGHEDCNGRMPNIAKVETKMDRRDRGDEDEEIDYTLCFRVRKMDIVYKPDWCEVRE

## IIIS1

hCavT1a SWSAYIFPPQSRFRLLCHRIITHRMFDHVVVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGL  
rCavT1a SWSAYIFPPQSRFRLLCHRIITHRMFDHVVVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGL  
hCavT2a PSTLYLESPQNRFRVSCQKVITHRMFDHVVVLIIFLNCITIALERPDIIDPGSTERVFLSVSNYIFTAIFVAEMVMKVVALGLLSGEHAYLQSSWNLLDGL  
hCavT3 DWSVYLESPENRFRVLCQTIIAHKLEFDVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVSLGLYFGEQAYLRSSWNVLDGF  
rCavT3 DWSVYLESPENKFRILCQTIIAHKLEFDVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVSLGLYFGEQAYLRSSWNVLDGF

## IIIS2

hCavT1a SWSAYIFPPQSRFRLLCHRIITHRMFDHVVVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGL  
rCavT1a SWSAYIFPPQSRFRLLCHRIITHRMFDHVVVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGL  
hCavT2a PSTLYLESPQNRFRVSCQKVITHRMFDHVVVLIIFLNCITIALERPDIIDPGSTERVFLSVSNYIFTAIFVAEMVMKVVALGLLSGEHAYLQSSWNLLDGL  
hCavT3 DWSVYLESPENRFRVLCQTIIAHKLEFDVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVSLGLYFGEQAYLRSSWNVLDGF  
rCavT3 DWSVYLESPENKFRILCQTIIAHKLEFDVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVSLGLYFGEQAYLRSSWNVLDGF

## IIIS4

hCavT1a LVLISVIDILVSMVSDSGTKILGMLRVLLRLTLRPLRVI SRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
rCavT1a LVLISVIDILVSMVSDSGTKILGMLRVLLRLTLRPLRVI SRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
hCavT2a LVLVSLVDIVVAMASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
hCavT3 LVFVSIIDIVVSLASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
rCavT3 LVFVSIIDIVVSVASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK

## IIIS5

hCavT1a LVLISVIDILVSMVSDSGTKILGMLRVLLRLTLRPLRVI SRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
rCavT1a LVLISVIDILVSMVSDSGTKILGMLRVLLRLTLRPLRVI SRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
hCavT2a LVLVSLVDIVVAMASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
hCavT3 LVFVSIIDIVVSLASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  
rCavT3 LVFVSIIDIVVSVASAGGAKILGVLRLRLTLRPLRVI SRAQGLKLVVETLSSLRPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK

Fig. 1C

IIIP LOOP IIIIS6

hCavT1a SDCAEASRWRHRYKYNFDNLGQALMSFLVASKDGVDDIMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKRCRQHQEAAA  
rCavT1a SDCAEASRWRHRYKYNFDNLGQALMSFLVASKDGVDDIMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKRCRQHQEAAA  
hCavT2a AQCAAHYRWRHRYKYNFDNLGQALMSFLVSSKDGWNIMYDGLDAVGVDQQPQNHNPMWMLLYFISFLLIVSFFVLNMFVGVVVENFHKRCRPHQEAAA  
hCavT3 SDCMAANYRWRHRYKYNFDNLGQALMSFLVASKDGVNIMYNGLDAAVDDQQPVTNHNPMWMLLYFISFLLIVSFFVLNMFVGVVVENFHKRCRQHQEAAA  
rCavT3 SDCVAANYRWRHRYKYNFDNLGQALMSFLVASKDGVNIMYNGLDAAVDDQQPVTNHNPMWMLLYFISFLLIVSFFVLNMFVGVVVENFHKRCRQHQEAAA

IVS1 IVS2

hCavT1a RREEKRLRRLRLEKKRRSKEKQMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLDFITGVIGLNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKL  
rCavT1a RREEKRLRRLRLEKKRRSKEKQMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLDFITGVIGLNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKL  
hCavT2a RREEKRLRRLRLEKRRR-STEPSPEAQRPPYADYSPTRRWIHSLCTSHYLDLDFITFIICNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAAKL  
hCavT3 RREEKRLRRLRLEKRR-K-----AQLPPYATYCTHRLLIHSMCTSHYLDLDFITFIICNVITMSLEHYNQPTSLETALKYCNYMFTTIVFVLEAVLKL  
rCavT3 RREEKRLRRLRLEKRR-K-----AQLPPYATYCTHRLLIHSMCTSHYLDLDFITFIICNVITMSLEHYNQPTSLETALKYCNYMFTTIVFVLEAVLKL

IVS3 IVS4 IVS5

hCavT1a AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVE  
rCavT1a AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVE  
hCavT2a AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVE  
hCavT3 AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVE  
rCavT3 AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVE

IVP LOOP IVS6

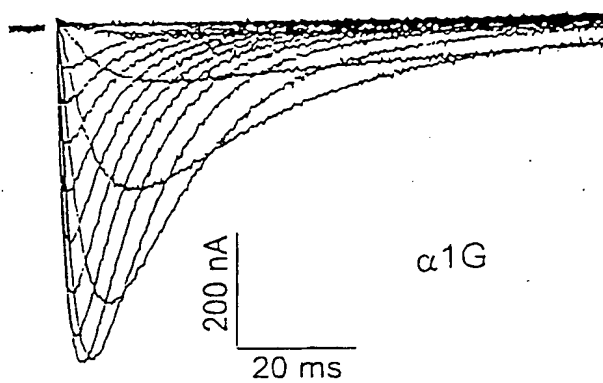
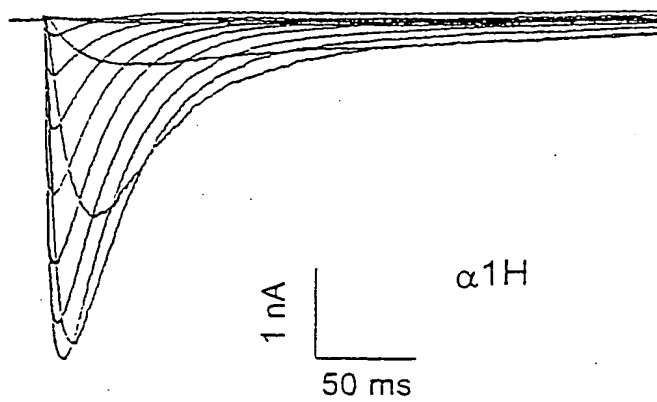
hCavT1a LFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDQDQEST---CYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLHEESNKE  
rCavT1a LFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDQDQEST---CYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLHEESNKE  
hCavT2a LFGRLCEDNPCEGLSRHATFSNFGMAFLTFRVSTGDNWNGIMKDTLRDQDQEST---CYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLHEESNKE  
hCavT3 LFGKLVNDENPCGMSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDQDQEST---CYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLHEESNKE  
rCavT3 LFGKLVNDENPCGMSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDQDQEST---CYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLHEESNKE

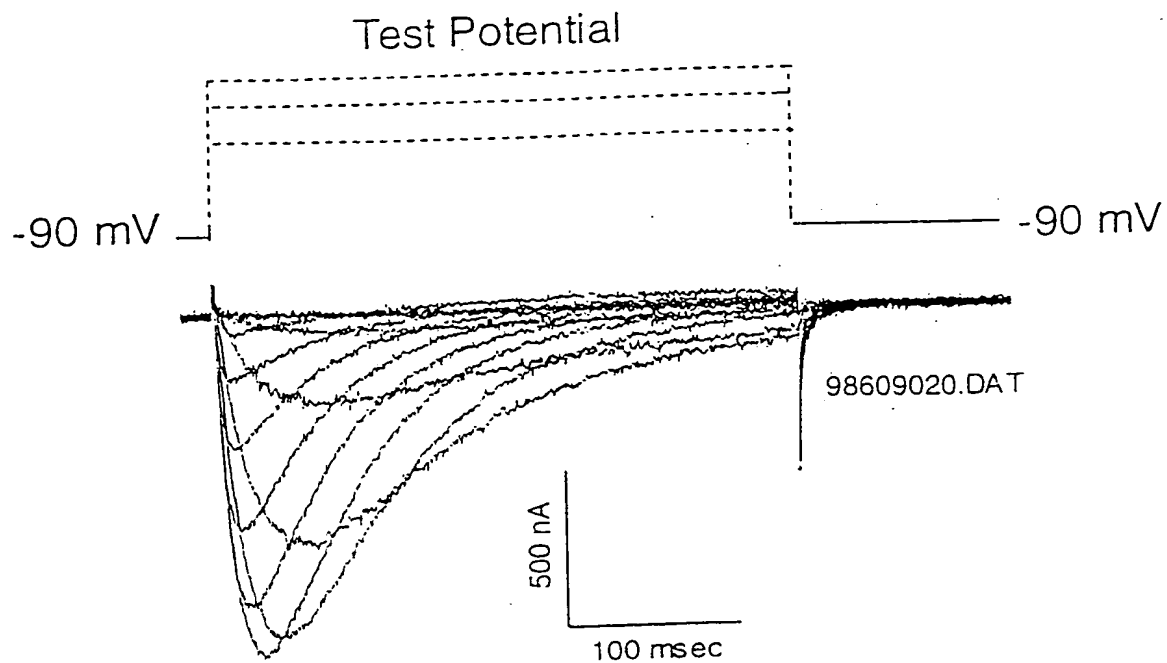
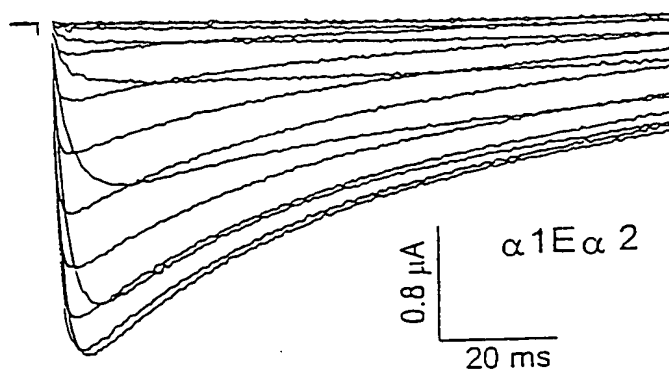
hCavT1a AKEEALEAELELEMTLSPQPHSPGLSPFPLWPGVGDSPDPSKPGALHPAAHARSASHFSLHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPND  
rCavT1a AKEEALEAELELEMTLSPQPHSPGLSPFPLWPGVGDSPDPSKPGALHPAAHARSASHFSLHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPND  
hCavT2a AREDAELDAEIELEMAQPGSARRV-----DADRPPLPQESPGARDAPNLVARKVSVSRMLSLPND  
hCavT3 AQEDAEMDAEIELEMAHGLGP-----  
rCavT3 AQEDAEMDAEIELEMAHGLGP-----

Fig. 1D

hCa<sub>v</sub>T1a SYMCRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTPKLPFGSPPLAQRPLRRQAAIRTDLSLDVQGLGSRE  
rCa<sub>v</sub>T1a SYMCRNGSTAERSLGRGWLGPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPFGSPPLAQRPLRRQAAIRTDLSLDVQGLGSRE  
hCa<sub>v</sub>T2a SYMERPVWPASAPHRPRLQEVEMETYGAGTPLGSAVSHSPPAESCASLQIPLAVSSPARSGE-----  
hCa<sub>v</sub>T3 -----GPRLPTGSPGAPGRGPGGAGGGDTGGILCRRCYSPAQENLWLDVSLIIKDS-----  
rCa<sub>v</sub>T3 -----GPRLPTSSPGAPGRGSGGAGAGGDTESHLCRHCYSPAQETLWLDVSLIIKDS-----  
  
hCa<sub>v</sub>T1a DLLAEVSGSPPLARAYFWGQSSTQAQHSRSHSKISKHMTTPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDLLPPGGQEEPPSPRDLKKCYSE  
rCa<sub>v</sub>T1a DLLSEVSGPSCPLTRSSFWGGSSIQVQORSIGQSKVSKHIRLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDLLPSS-QEEPLEFRDLKKCYSE  
hCa<sub>v</sub>T2a -----PLHALSPRGRTARSPSLRLLCRQEAHVTDLSLKGRLTALGTFTWILQSLVRKPR (SEQ ID NO:9)  
hCa<sub>v</sub>T3 -----LEGELTIIDNLGSIFFHYSSPAGCKKCHDKQETGPRPSCWTT (SEQ ID NO:11)  
rCa<sub>v</sub>T3 -----LEGELTIIDNLGSIFFHYASPDGCGKCHDKQETGLHPSCWGMT (SEQ ID NO:12)  
  
hCa<sub>v</sub>T1a AQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPNLSGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTPPSGICLRRRAPSSDKDPLASGPPD  
rCa<sub>v</sub>T1a TQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSLSGGQPLGGPGSRPKKKLSPPSISIDPPESQGSRRPPCSPGVCLRRRAPASDKDPSVSSPLD  
  
hCa<sub>v</sub>T1a SMAASPSPKOVLSLSGLSSDPADLDP (SEQ ID NO:1)  
rCa<sub>v</sub>T1a STAASPSPKOTLSLSGLSSDPTDMDP (SEQ ID NO:5)

Fig. 1E

**Figure 2A****Figure 2B**

**Figure 2C****Figure 2D**

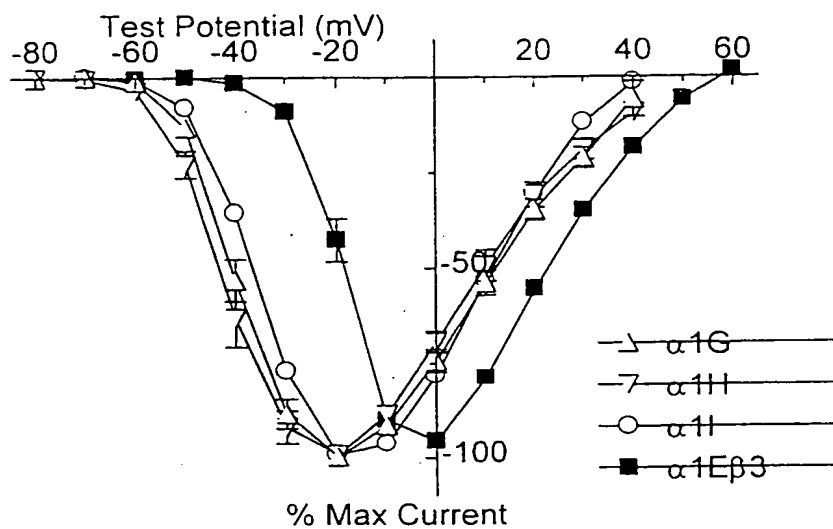


Figure 3A

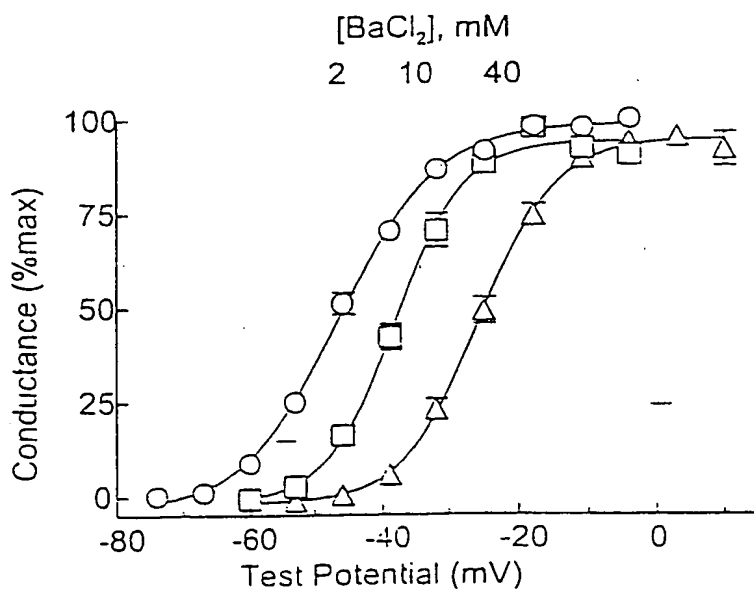
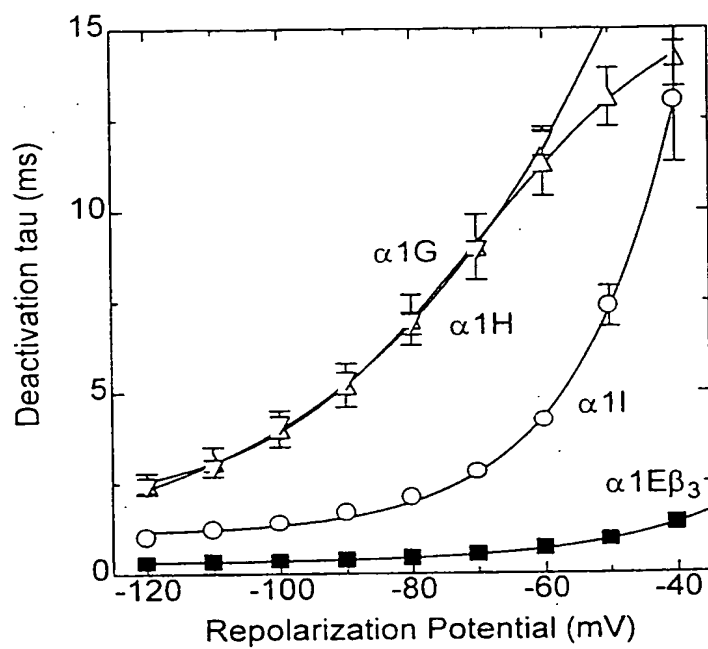
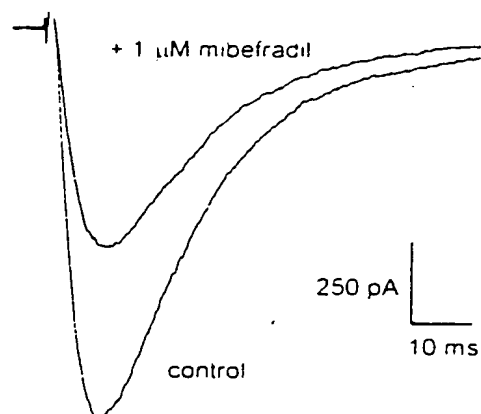
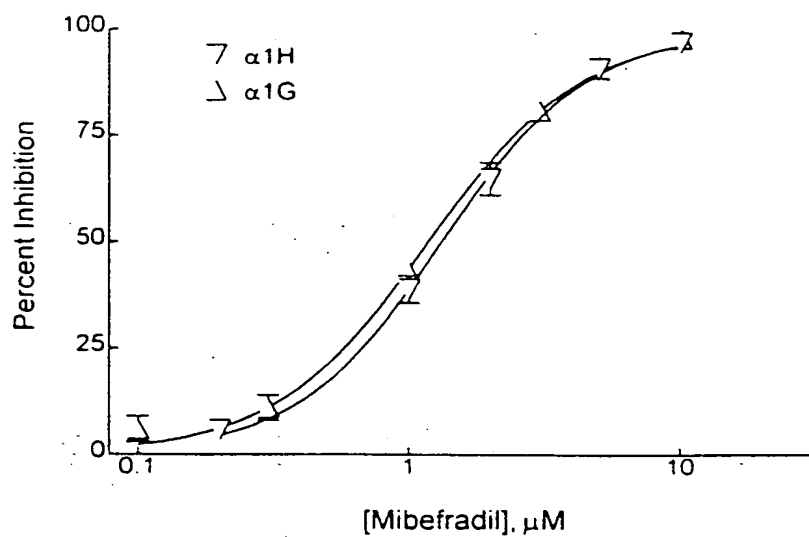


Figure 3B



**Figure 4**

**Figure 5A****Figure 5B**

## SEQUENCE LISTING

5 <110> Perez-Reyes, Edward  
 Cribbs, Leanne L.  
 Loyola University of Chicago

<120> T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF  
 USING SAME

10 <130> 89066

<140>  
 <141>

15 <150> US 08/985,809  
 <151> 1997-12-05

<160> 13

20 <170> PatentIn Ver. 2.0

<210> 1  
 <211> 6750  
 <212> DNA

25 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(6750)

30 <400> 1

atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc	48
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro	
1 5 10 15	
35 cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg	96
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro	
20 25 30	
40 ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg	144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala	
35 40 45	
45 gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg	192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu	
50 55 60	
50 agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac	240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn	
65 70 75 80	
ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg	288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val	
85 90 95	
55 acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag	336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln	
100 105 110	
60 cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt	384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe	
115 120 125	
gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa	432

	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	
	130						135					140					
5	aag	tgt	tac	ctg	gga	gac	act	tgg	aac	cgg	ctt	gac	ttt	ttc	atc	gtc	480
	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val	
	145					150					155					160	
10	atc	gca	ggg	atg	ctg	gag	tac	tgc	ctg	gac	ctg	cag	aac	gtc	agc	ttc	528
	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe	
					165					170					175		
15	tca	gct	gtc	agg	aca	gtc	cgt	gtg	ctg	cga	ccg	ctc	agg	gcc	att	aac	576
	Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn	
				180					185					190			
20	cgg	gtg	ccc	agc	atg	cgc	atc	ctt	gtc	acg	ttg	ctg	ctg	gat	acg	ctg	624
	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu	
			195					200					205				
25	ccc	atg	ctg	ggc	aac	gtc	ctg	ctg	ctc	tgc	ttc	ttc	gtc	ttc	ttc	atc	672
	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	
		210					215					220					
30	ttc	ggc	atc	gtc	ggc	gtc	cag	ctg	tgg	gca	ggg	ctg	ctt	cgg	aac	cga	720
	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	
	225					230					235					240	
35	tgc	ttc	cta	cct	gag	aat	ttc	agc	ctc	ccc	ctg	agc	gtg	gac	ctg	gag	768
	Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu	
					245					250					255		
40	cgc	tat	tac	cag	aca	gag	aac	gag	gat	gag	agc	ccc	ttc	atc	tgc	tcc	816
	Arg	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser	
				260					265					270			
45	cag	cca	cgc	gag	aac	ggc	atg	cgg	tcc	tgc	aga	agc	gtg	ccc	acg	ctg	864
	Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu	
			275					280					285				
50	cgc	ggg	gac	ggg	ggc	ggt	ggc	cca	cct	tgc	ggt	ctg	gac	tat	gag	gcc	912
	Arg	Gly	Asp	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Gly	Leu	Asp	Tyr	Glu	Ala	
		290				295						300					
55	tac	aac	agc	tcc	agc	aac	acc	acc	tgt	gtc	aac	tgg	aac	cag	tac	tac	960
	Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr	
	305					310					315					320	
60	acc	aac	tgc	tca	gcg	ggg	gag	cac	aac	ccc	ttc	aag	ggc	gcc	atc	aac	1008
	Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn	
					325					330					335		
65	ttt	gac	aac	att	ggc	tat	gcc	tgg	atc	gcc	atc	ttc	cag	gtc	atc	acg	1056
	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr	
				340				345						350			
70	ctg	gag	ggc	tgg	gtc	gac	atc	atg	tac	ttt	gtg	atg	gat	gct	cat	tcc	1104
	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser	
			355					360					365				
75	ttc	tac	aat	ttc	atc	tac	ttc	atc	ctc	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
		370					375					380					
80	ttc	atg	atc	aac	ctg	tgc	ctg	gtg	gtg	att	gcc	acg	cag	ttc	tca	gag	1200

	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu	
	385					390					395					400	
5	acc	aag	cag	cgg	gaa	agc	cag	ctg	atg	cgg	gag	cag	cgt	gtg	cgg	ttc	1248
	Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe	
					405					410					415		
10	ctg	tcc	aac	gcc	agc	acc	ctg	gct	agc	ttc	tct	gag	ccc	ggc	agc	tgc	1296
	Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys	
				420					425					430			
15	tat	gag	gag	ctg	ctc	aag	tac	ctg	gtg	tac	atc	ctt	cgt	aag	gca	gcc	1344
	Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala	
			435					440					445				
	cgc	agg	ctg	gct	cag	gtc	tct	cgg	gca	gca	ggg	gtg	cgg	gtt	ggg	ctg	1392
	Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ala	Gly	Val	Arg	Val	Gly	Leu	
		450					455					460					
20	ctc	agc	agc	cca	gca	ccc	ctc	ggg	ggc	cag	gag	acc	cag	ccc	agc	agc	1440
	Leu	Ser	Ser	Pro	Ala	Pro	Leu	Gly	Gly	Gln	Glu	Thr	Gln	Pro	Ser	Ser	
	465					470					475					480	
25	agc	tgc	tct	cgc	tcc	cac	cgc	cgc	cta	tcc	gtc	cac	cac	ctg	gtg	cac	1488
	Ser	Cys	Ser	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His	
					485					490					495		
30	cac	cac	cac	cac	cat	cac	cac	cac	tac	cac	ctg	ggc	aat	ggg	acg	ctc	1536
	His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu	
				500					505					510			
35	agg	gcc	ccc	cgg	gcc	agc	ccg	gag	atc	cag	gac	agg	gat	gcc	aat	ggg	1584
	Arg	Ala	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly	
			515					520					525				
	tcc	cgc	cgg	ctc	atg	ctg	cca	cca	ccc	tgc	acg	cct	gcc	ctc	tcc	ggg	1632
	Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr		Ala	Leu	Ser	Gly	
		530					535					540					
40	gcc	ccc	cct	ggg	ggc	gca	gag	tct	gtg	cac	agc	ttc	tac	cat	gcc	gac	1680
	Ala	Pro	Pro	Gly	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp	
	545					550					555					560	
45	tgc	cac	tta	gag	cca	gtc	cgc	tgc	cag	gcg	ccc	cct	ccc	agg	tcc	cca	1728
	Cys	His	Leu	Glu	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Ser	Pro	
					565					570					575		
50	tct	gag	gca	tcc	ggc	agg	act	gtg	ggc	agc	ggg	aag	gtg	tat	ccc	acc	1776
	Ser	Glu	Ala	Ser	Gly	Arg	Thr	Val	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr	
				580					585					590			
55	gtg	cac	acc	agc	cct	cca	ccg	gag	acg	ctg	aag	gag	aag	gca	cta	gta	1824
	Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Thr	Leu	Lys	Glu	Lys	Ala	Leu	Val	
			595					600					605				
	gag	gtg	gct	gcc	agc	tct	ggg	ccc	cca	acc	ctc	acc	agc	ctc	aac	atc	1872
	Glu	Val	Ala	Ala	Ser	Ser	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Leu	Asn	Ile	
		610					615					620					
60	cca	ccc	ggg	ccc	tac	agc	tcc	atg	cac	aag	ctg	ctg	gag	aca	cag	agt	1920
	Pro	Pro	Gly	Pro	Tyr	Ser	Ser	Met	His	Lys	Leu	Leu	Glu	Thr	Gln	Ser	
	625					630					635					640	
	aca	ggg	gcc	tgc	caa	agc	tct	tgc	aag	atc	tcc	agc	cct	tgc	ttg	aaa	1968

	Thr	Gly	Ala	Cys	Gln	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Leu	Lys	
					645					650					655		
5	gca	gac	agt	gga	gcc	tgt	ggc	cca	gac	agc	tgc	ccc	tac	tgt	gcc	cgg	2016
	Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pro	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg	
				660				665						670			
10	gcc	ggg	gca	ggg	gag	gtg	gag	ctc	gcc	gac	cgt	gaa	atg	cct	gac	tca	2064
	Ala	Gly	Ala	Gly	Glu	Val	Glu	Leu	Ala	Asp	Arg	Glu	Met	Pro	Asp	Ser	
				675				680					685				
15	gac	agc	gag	gca	gtt	tat	gag	ttc	aca	cag	gat	gcc	cag	cac	agc	gac	2112
	Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp	
				690			695					700					
20	ctc	cgg	gac	ccc	cac	agc	cgg	cgg	caa	cgg	agc	ctg	ggc	cca	gat	gca	2160
	Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	Ala	
						710					715					720	
25	gag	ccc	agc	tct	gtg	ctg	gcc	ttc	tgg	agg	cta	atc	tgt	gac	acc	ttc	2208
	Glu	Pro	Ser	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	Phe	
					725				730						735		
30	cga	aag	att	gtg	gac	agc	aag	tac	ttt	ggc	cgg	gga	atc	atg	atc	gcc	2256
	Arg	Lys	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	Ala	
				740				745						750			
35	atc	ctg	gtc	aac	aca	ctc	agc	atg	ggc	atc	gaa	tac	cac	gag	cag	ccc	2304
	Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	Glu	Tyr	His	Glu	Gln	Pro	
				755				760					765				
40	gag	gag	ctt	acc	aac	gcc	cta	gaa	atc	agc	aac	atc	gtc	ttc	acc	agc	2352
	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr	Ser	
				770			775					780					
45	ctc	ttt	gcc	ctg	gag	atg	ctg	ctg	aag	ctg	ctt	gtg	tat	ggc	ccc	ttt	2400
	Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	Phe	
						790					795					800	
50	ggc	tac	atc	aag	aat	ccc	tac	aac	atc	ttc	gat	ggc	gtc	att	gtg	gtc	2448
	Gly	Tyr	Ile	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	Val	
					805					810					815		
55	atc	agc	gtg	tgg	gag	atc	gtg	ggc	cag	cag	ggg	ggc	ggc	ctg	tcg	gtg	2496
	Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser	Val	
				820				825						830			
60	ctg	cgg	acc	ttc	cgc	ctg	atg	cgt	gtg	ctg	aag	ctg	gtg	cgc	ttc	ctg	2544
	Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	Leu	
				835				840					845				
65	cgc	gcg	ctg	cag	cgg	cag	ctg	gtg	gtg	ctc	atg	aag	acc	atg	gac	aac	2592
	Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	Asn	
				850			855					860					
70	gtg	gcc	acc	ttc	tgc	atg	ctg	ctt	atg	ctc	ttc	atc	ttc	atc	ttc	agc	2640
	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	Ser	
						870				875						880	
75	atc	ctg	ggc	atg	cat	ctc	ttc	ggc	tgc	aag	ttt	gcc	tct	gag	cgg	gat	2688
	Ile	Leu	Gly	Met	His	Leu	Phe	Gly	Cys	Lys	Phe	Ala	Ser	Glu	Arg	Asp	
					885					890					895		
80	ggg	gac	acc	ctg	cca	gac	cgg	aag	aat	ttt	gac	tcc	ttg	ctc	tgg	gcc	2736

	Gly	Asp	Thr	Leu	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp	Ala	
				900					905					910			
5	atc	gtc	act	gtc	ttt	cag	atc	ctg	acc	cag	gag	gac	tgg	aac	aaa	gtc	2784
	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Lys	Val	
				915				920					925				
10	ctc	tac	aat	ggt	atg	gcc	tcc	acg	tcg	tcc	tgg	gcg	gcc	ctt	tat	ttc	2332
	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr	Phe	
				930			935					940					
15	att	gcc	ctc	atg	acc	ttc	ggc	aac	tac	gtg	ctc	ttc	aat	ttg	ctg	gtc	2880
	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	Val	
						950					955					960	
	gcc	att	ctg	gtg	gag	ggc	ttc	cag	gcg	gag	gga	gat	gcc	aac	aag	tcc	2928
	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Gly	Asp	Ala	Asn	Lys	Ser	
					965					970					975		
20	gaa	tca	gag	ccc	gat	ttc	ttc	tca	ccc	agc	ctg	gat	ggt	gat	ggg	gac	2976
	Glu	Ser	Glu	Pro	Asp	Phe	Phe	Ser	Pro	Ser	Leu	Asp	Gly	Asp	Gly	Asp	
				980					985					990			
25	agg	aag	aag	tgc	ttg	gcc	ttg	gtg	tcc	ctg	gga	gag	cac	ccg	gag	ctg	3024
	Arg	Lys	Lys	Cys	Leu	Ala	Leu	Val	Ser	Leu	Gly	Glu	His	Pro	Glu	Leu	
			995					1000					1005				
30	cgg	aag	agc	ctg	ctg	ccg	cct	ctc	atc	atc	cac	acg	gcc	gcc	aca	ccc	3072
	Arg	Lys	Ser	Leu	Leu	Pro	Pro	Leu	Ile	Ile	His	Thr	Ala	Ala	Thr	Pro	
		1010					1015					1020					
35	atg	tcg	ctg	ccc	aag	agc	acc	agc	acg	ggc	ctg	ggc	gag	gcg	ctg	ggc	3120
	Met	Ser	Leu	Pro	Lys	Ser	Thr	Ser	Thr	Gly	Leu	Gly	Glu	Ala	Leu	Gly	
		1025				1030					1035					1040	
	cct	gcg	tcg	cgc	cgc	acc	agc	agc	agc	ggg	tcg	gca	gag	cct	ggg	gcg	3168
	Pro	Ala	Ser	Arg	Arg	Thr	Ser	Ser	Ser	Gly	Ser	Ala	Glu	Pro	Gly	Ala	
					1045					1050					1055		
40	gcc	cac	gag	atg	aag	tca	ccg	ccc	agc	gcc	cgc	agc	tct	ccg	cac	agc	3216
	Ala	His	Glu	Met	Lys	Ser	Pro	Pro	Ser	Ala	Arg	Ser	Ser	Pro	His	Ser	
				1060					1065					1070			
45	ccc	tgg	agc	gct	gca	agc	agc	tgg	acc	agc	agg	cgc	tcc	agc	cgg	aac	3264
	Pro	Trp	Ser	Ala	Ala	Ser	Ser	Trp	Thr	Ser	Arg	Arg	Ser	Ser	Arg	Asn	
			1075					1080					1085				
50	agc	ctc	ggc	cgt	gca	ccc	agc	ctg	aag	cgg	aga	agc	cca	agt	gga	gag	3312
	Ser	Leu	Gly	Arg	Ala	Pro	Ser	Leu	Lys	Arg	Arg	Ser	Pro	Ser	Gly	Glu	
		1090					1095					1100					
55	cgg	cgg	tcc	ctg	ttg	tcg	gga	gaa	ggc	cag	gag	agc	cag	gat	gaa	gag	3360
	Arg	Arg	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gln	Glu	Ser	Gln	Asp	Glu	Glu	
		1105				1110					1115					1120	
	gag	agc	tca	gaa	gag	gag	cgg	gcc	agc	cct	gcg	ggc	agt	gac	cat	cgc	3408
	Glu	Ser	Ser	Glu	Glu	Glu	Arg	Ala	Ser	Pro	Ala	Gly	Ser	Asp	His	Arg	
				1125					1130						1135		
60	cac	agg	ggg	tcc	ctg	gag	cgg	gag	gcc	aag	agt	tcc	ttt	gac	ctg	cca	3456
	His	Arg	Gly	Ser	Leu	Glu	Arg	Glu	Ala	Lys	Ser	Ser	Phe	Asp	Leu	Pro	
				1140					1145					1150			
	gac	aca	ctg	cag	gtg	cca	ggg	ctg	cat	cgc	act	gcc	agt	ggc	cga	ggg	3504

	Asp	Thr	Leu	Gln	Val	Pro	Gly	Leu	His	Arg	Thr	Ala	Ser	Gly	Arg	Gly	
	1155						1160						1165				
5	tct	gct	tct	gag	cac	cag	gac	tgc	aat	ggc	aag	tgc	gct	tca	ggg	cgc	3552
	Ser	Ala	Ser	Glu	His	Gln	Asp	Cys	Asn	Gly	Lys	Ser	Ala	Ser	Gly	Arg	
	1170					1175					1180						
10	ctg	gcc	cgg	gcc	ctg	cgg	cct	gat	gac	ccc	cca	ctg	gat	ggg	gat	gac	3600
	Leu	Ala	Arg	Ala	Leu	Arg	Pro	Asp	Asp	Pro	Pro	Leu	Asp	Gly	Asp	Asp	
	1185				1190					1195						1200	
15	gcc	gat	gac	gag	ggc	aac	ctg	agc	aaa	ggg	gaa	cgg	gtc	cgc	ggg	tgg	3648
	Ala	Asp	Asp	Glu	Gly	Asn	Leu	Ser	Lys	Gly	Glu	Arg	Val	Arg	Ala	Trp	
				1205					1210					1215			
	atc	cga	gcc	cga	ctc	cct	gcc	tgc	tgc	ctc	gag	cga	gac	tcc	tgg	tca	3696
	Ile	Arg	Ala	Arg	Leu	Pro	Ala	Cys	Cys	Leu	Glu	Arg	Asp	Ser	Trp	Ser	
				1220				1225					1230				
20	gcc	tac	atc	ttc	cct	cct	cag	tcc	agg	ttc	cgc	ctc	ctg	tgt	cac	cgg	3744
	Ala	Tyr	Ile	Phe	Pro	Pro	Gln	Ser	Arg	Phe	Arg	Leu	Leu	Cys	His	Arg	
		1235					1240					1245					
25	atc	atc	acc	cac	aag	atg	ttc	gac	cac	gtg	gtc	ctt	gtc	atc	atc	ttc	3792
	Ile	Ile	Thr	His	Lys	Met	Phe	Asp	His	Val	Val	Leu	Val	Ile	Ile	Phe	
	1250					1255					1260						
30	ctt	aac	tgc	atc	acc	atc	gcc	atg	gag	cgc	ccc	aaa	att	gac	ccc	cac	3840
	Leu	Asn	Cys	Ile	Thr	Ile	Ala	Met	Glu	Arg	Pro	Lys	Ile	Asp	Pro	His	
	1265			1270						1275					1280		
35	agc	gct	gaa	cgc	atc	ttc	ctg	acc	ctc	tcc	aat	tac	atc	ttc	acc	gca	3888
	Ser	Ala	Glu	Arg	Ile	Phe	Leu	Thr	Leu	Ser	Asn	Tyr	Ile	Phe	Thr	Ala	
				1285					1290					1295			
	gtc	ttt	ctg	gct	gaa	atg	aca	gtg	aag	gtg	gtg	gca	ctg	ggc	tgg	tgc	3936
	Val	Phe	Leu	Ala	Glu	Met	Thr	Val	Lys	Val	Val	Ala	Leu	Gly	Trp	Cys	
			1300					1305					1310				
40	ttc	ggg	gag	cag	gcg	tac	ctg	cgg	agc	agt	tgg	aac	gtg	ctg	gac	ggg	3984
	Phe	Gly	Glu	Gln	Ala	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	Val	Leu	Asp	Gly	
		1315					1320					1325					
45	ctg	ttg	gtg	ctc	atc	tcc	gtc	atc	gac	att	ctg	gtg	tcc	atg	gtc	tct	4032
	Leu	Leu	Val	Leu	Ile	Ser	Val	Ile	Asp	Ile	Leu	Val	Ser	Met	Val	Ser	
	1330				1335						1340						
50	gac	agc	ggc	acc	aag	atc	ctg	ggc	atg	ctg	agg	gtg	ctg	cgg	ctg	ctg	4080
	Asp	Ser	Gly	Thr	Lys	Ile	Leu	Gly	Met	Leu	Arg	Val	Leu	Arg	Leu	Leu	
	1345			1350						1355					1360		
55	cgg	acc	ctg	cgc	ccg	ctc	agg	gtg	atc	agc	cgg	gcg	cag	ggg	ctg	aag	4128
	Arg	Thr	Leu	Arg	Pro	Leu	Arg	Val	Ile	Ser	Arg	Ala	Gln	Gly	Leu	Lys	
				1365				1370						1375			
	ctg	gtg	gtg	gag	acg	ctg	atg	tcc	tca	ctg	aaa	ccc	atc	ggc	aac	att	4176
	Leu	Val	Val	Glu	Thr	Leu	Met	Ser	Ser	Leu	Lys	Pro	Ile	Gly	Asn	Ile	
			1380				1385						1390				
60	gta	gtc	atc	tgc	tgt	gcc	ttc	ttc	atc	att	ttc	ggc	atc	ttg	ggg	gtg	4224
	Val	Val	Ile	Cys	Cys	Ala	Phe	Phe	Ile	Ile	Phe	Gly	Ile	Leu	Gly	Val	
		1395				1400					1405						
	cag	ctc	ttc	aaa	ggg	aag	ttt	ttc	gtg	tgc	cag	ggc	gag	gat	acc	agg	4272



	Gln	Leu	Phe	Lys	Gly	Lys	Phe	Phe	Val	Cys	Gln	Gly	Glu	Asp	Thr	Arg	
	1410					1415					1420						
5	aac	atc	acc	aat	aaa	tcg	gac	tgt	gcc	gag	gcc	agt	tac	cgg	tgg	gtc	4320
	Asn	Ile	Thr	Asn	Lys	Ser	Asp	Cys	Ala	Glu	Ala	Ser	Tyr	Arg	Trp	Val	
	1425				1430				1435						1440		
10	cgg	cac	aag	tac	aac	ttt	gac	aac	ctt	ggc	cag	gcc	ctg	atg	tcc	ctg	4368
	Arg	His	Lys	Tyr	Asn	Phe	Asp	Asn	Leu	Gly	Gln	Ala	Leu	Met	Ser	Leu	
				1445					1450					1455			
15	ttc	gtt	ttg	gcc	tcc	aag	gat	ggt	tgg	gtg	gac	atc	atg	tac	gat	ggg	4416
	Phe	Val	Leu	Ala	Ser	Lys	Asp	Gly	Trp	Val	Asp	Ile	Met	Tyr	Asp	Gly	
		1460						1465					1470				
	ctg	gat	gct	gtg	ggc	gtg	gac	cag	cag	ccc	atc	atg	aac	cac	aac	ccc	4464
	Leu	Asp	Ala	Val	Gly	Val	Asp	Gln	Gln	Pro	Ile	Met	Asn	His	Asn	Pro	
		1475					1480					1485					
20	tgg	atg	ctg	ctg	tac	ttc	atc	tcg	ttc	ctg	ctc	att	gtg	gcc	ttc	ttt	4512
	Trp	Met	Leu	Leu	Tyr	Phe	Ile	Ser	Phe	Leu	Leu	Ile	Val	Ala	Phe	Phe	
	1490					1495					1500						
25	gtc	ctg	aac	atg	ttt	gtg	ggt	gtg	gtg	gtg	gag	aac	ttc	cac	aag	tgt	4560
	Val	Leu	Asn	Met	Phe	Val	Gly	Val	Val	Val	Glu	Asn	Phe	His	Lys	Cys	
	1505				1510					1515					1520		
30	cgg	cag	cac	cag	gag	gaa	gag	gag	gcc	cgg	cgg	cgg	gag	gag	aag	cgc	4608
	Arg	Gln	His	Gln	Glu	Glu	Glu	Glu	Ala	Arg	Arg	Arg	Glu	Glu	Lys	Arg	
				1525					1530						1535		
35	cta	cga	aga	ctg	gag	aaa	aag	aga	agg	agt	aag	gag	aag	cag	atg	gct	4656
	Leu	Arg	Arg	Leu	Glu	Lys	Lys	Arg	Arg	Ser	Lys	Glu	Lys	Gln	Met	Ala	
			1540					1545					1550				
	gaa	gcc	cag	tgc	aaa	cct	tac	tac	tcc	gac	tac	tcc	cgc	ttc	cgg	ctc	4704
	Glu	Ala	Gln	Cys	Lys	Pro	Tyr	Tyr	Ser	Asp	Tyr	Ser	Arg	Phe	Arg	Leu	
		1555					1560					1565					
40	ctc	gtc	cac	cac	ttg	tgc	acc	agc	cac	tac	ctg	gac	ctc	ttc	atc	aca	4752
	Leu	Val	His	His	Leu	Cys	Thr	Ser	His	Tyr	Leu	Asp	Leu	Phe	Ile	Thr	
	1570					1575					1580						
45	ggt	gtc	atc	ggg	ctg	aac	gtg	gtc	acc	atg	gcc	atg	gag	cac	tac	cag	4800
	Gly	Val	Ile	Gly	Leu	Asn	Val	Val	Thr	Met	Ala	Met	Glu	His	Tyr	Gln	
	1585				1590				1595						1600		
50	cag	ccc	cag	att	ctg	gat	gag	gct	ctg	aag	atc	tgc	aac	tac	atc	ttc	4848
	Gln	Pro	Gln	Ile	Leu	Asp	Glu	Ala	Leu	Lys	Ile	Cys	Asn	Tyr	Ile	Phe	
			1605						1610					1615			
55	act	gtc	atc	ttt	gtc	ttg	gag	tca	gtt	ttc	aaa	ctt	gtg	gcc	ttt	ggt	4896
	Thr	Val	Ile	Phe	Val	Leu	Glu	Ser	Val	Phe	Lys	Leu	Val	Ala	Phe	Gly	
			1620				1625						1630				
	ttc	cgt	cgg	ttc	ttc	cag	gac	agg	tgg	aac	cag	ctg	gac	ctg	gcc	att	4944
	Phe	Arg	Arg	Phe	Phe	Gln	Asp	Arg	Trp	Asn	Gln	Leu	Asp	Leu	Ala	Ile	
		1635					1640					1645					
60	gtg	ctg	ctg	tcc	atc	atg	ggc	atc	acg	ctg	gag	gaa	atc	gag	gtc	aac	4992
	Val	Leu	Leu	Ser	Ile	Met	Gly	Ile	Thr	Leu	Glu	Glu	Ile	Glu	Val	Asn	
	1650					1655					1660						
	gcc	tcg	ctg	ccc	atc	aac	ccc	acc	atc	atc	cgc	atc	atg	agg	gtg	ctg	5040

	Ala	Ser	Leu	Pro	Ile	Asn	Pro	Thr	Ile	Ile	Arg	Ile	Met	Arg	Val	Leu	
	1665					1670					1675					1680	
5	cgc	att	gcc	cga	gtg	ctg	aag	ctg	ctg	aag	atg	gct	gtg	ggc	atg	cgg	5088
	Arg	Ile	Ala	Arg	Val	Leu	Lys	Leu	Leu	Lys	Met	Ala	Val	Gly	Met	Arg	
				1685						1690					1695		
10	gcg	ctg	ctg	gac	acg	gtg	atg	cag	gcc	ctg	ccc	cag	gtg	ggg	aac	ctg	5136
	Ala	Leu	Leu	Asp	Thr	Val	Met	Gln	Ala	Leu	Pro	Gln	Val	Gly	Asn	Leu	
				1700					1705					1710			
15	gga	ctt	ctc	ttc	atg	ttg	ttg	ttt	ttc	atc	ttt	gca	gct	ctg	ggc	gtg	5184
	Gly	Leu	Leu	Phe	Met	Leu	Leu	Phe	Phe	Ile	Phe	Ala	Ala	Leu	Gly	Val	
			1715					1720					1725				
	gag	ctc	ttt	gga	gac	ctg	gag	tgt	gac	gag	aca	cac	ccc	tgt	gag	ggc	5232
	Glu	Leu	Phe	Gly	Asp	Leu	Glu	Cys	Asp	Glu	Thr	His	Pro	Cys	Glu	Gly	
		1730					1735					1740					
20	ctg	ggc	cgt	cat	gcc	acc	ttt	cgg	aac	ttt	ggc	atg	gcc	ttc	cta	acc	5280
	Leu	Gly	Arg	His	Ala	Thr	Phe	Arg	Asn	Phe	Gly	Met	Ala	Phe	Leu	Thr	
		1745				1750					1755					1760	
25	ctc	ttc	cga	gtc	tcc	aca	ggt	gac	aat	tgg	aat	ggc	att	atg	aag	gac	5328
	Leu	Phe	Arg	Val	Ser	Thr	Gly	Asp	Asn	Trp	Asn	Gly	Ile	Met	Lys	Asp	
					1765					1770					1775		
30	acc	ctc	cgg	gac	tgt	gac	cag	gag	tcc	acc	tgc	tac	aac	acg	gtc	atc	5376
	Thr	Leu	Arg	Asp	Cys	Asp	Gln	Glu	Ser	Thr	Cys	Tyr	Asn	Thr	Val	Ile	
			1780						1785					1790			
35	tcg	cct	atc	tac	ttt	gtg	tcc	ttc	gtg	ctg	acg	gcc	cag	ttc	gtg	cta	5424
	Ser	Pro	Ile	Tyr	Phe	Val	Ser	Phe	Val	Leu	Thr	Ala	Gln	Phe	Val	Leu	
			1795					1800					1805				
	gtc	aac	gtg	gtg	atc	gcc	gtg	ctg	atg	aag	cac	ctg	gag	gag	agc	aac	5472
	Val	Asn	Val	Val	Ile	Ala	Val	Leu	Met	Lys	His	Leu	Glu	Glu	Ser	Asn	
		1810					1815					1820					
40	aag	gag	gcc	aag	gag	gag	gcc	gag	cta	gag	gct	gag	ctg	gag	ctg	gag	5520
	Lys	Glu	Ala	Lys	Glu	Glu	Ala	Glu	Leu	Glu	Ala	Glu	Leu	Glu	Leu	Glu	
		1825				1830					1835					1840	
45	atg	aag	acc	ctc	agc	ccc	cag	ccc	cac	tcg	cca	ctg	ggc	agc	ccc	ttc	5568
	Met	Lys	Thr	Leu	Ser	Pro	Gln	Pro	His	Ser	Pro	Leu	Gly	Ser	Pro	Phe	
					1845					1850					1855		
50	ctc	tgg	cct	ggg	gtc	gag	ggc	ccc	gac	agc	ccc	gac	agc	ccc	aag	cct	5616
	Leu	Trp	Pro	Gly	Val	Glu	Gly	Pro	Asp	Ser	Pro	Asp	Ser	Pro	Lys	Pro	
			1860					1865					1870				
55	ggg	gct	ctg	cac	cca	gcg	gcc	cac	gcg	aga	tca	gcc	tcc	cac	ttt	tcc	5664
	Gly	Ala	Leu	His	Pro	Ala	Ala	His	Ala	Arg	Ser	Ala	Ser	His	Phe	Ser	
			1875					1880					1885				
	ctg	gag	cac	ccc	acg	atg	cag	ccc	cac	ccc	acg	gag	ctg	cca	gga	cca	5712
	Leu	Glu	His	Pro	Thr	Met	Gln	Pro	His	Pro	Thr	Glu	Leu	Pro	Gly	Pro	
		1890					1895					1900					
60	gac	tta	ctg	act	gtg	cgg	aag	tct	ggg	gtc	agc	cga	acg	cac	tct	ctg	5760
	Asp	Leu	Leu	Thr	Val	Arg	Lys	Ser	Gly	Val	Ser	Arg	Thr	His	Ser	Leu	
		1905				1910					1915					1920	
	ccc	aat	gac	agc	tac	atg	tgt	cgg	cat	ggg	agc	act	gcc	gag	ggg	ccc	5808

	Pro	Asn	Asp	Ser	Tyr	Met	Cys	Arg	His	Gly	Ser	Thr	Ala	Glu	Gly	Pro	
				1925						1930					1935		
5	ctg	gga	cac	agg	ggc	tgg	ggg	ctc	ccc	aaa	gct	cag	tca	ggc	tcc	gtc	5556
	Leu	Gly	His	Arg	Gly	Trp	Gly	Leu	Pro	Lys	Ala	Gln	Ser	Gly	Ser	Val	
				1940				1945					1950				
10	ttg	tcc	ggt	cac	tcc	cag	cca	gca	gat	acc	agc	tac	atc	ctg	cag	ctt	5904
	Leu	Ser	Val	His	Ser	Gln	Pro	Ala	Asp	Thr	Ser	Tyr	Ile	Leu	Gln	Leu	
				1955				1960					1965				
15	ccc	aaa	gat	gca	cct	cat	ctg	ctc	cag	ccc	cac	agc	gcc	cca	acc	tgg	5952
	Pro	Lys	Asp	Ala	Pro	His	Leu	Leu	Gln	Pro	His	Ser	Ala	Pro	Thr	Trp	
				1970				1975					1980				
	ggc	acc	atc	ccc	aaa	ctg	ccc	cca	cca	gga	cgc	tcc	cct	ttg	gct	cag	6000
	Gly	Thr	Ile	Pro	Lys	Leu	Pro	Pro	Pro	Gly	Arg	Ser	Pro	Leu	Ala	Gln	
				1985				1990				1995				2000	
20	agg	cca	ctc	agg	cgc	cag	gca	gca	ata	agg	act	gac	tcc	ttg	gac	ggt	6048
	Arg	Pro	Leu	Arg	Arg	Gln	Ala	Ala	Ile	Arg	Thr	Asp	Ser	Leu	Asp	Val	
						2005					2010					2015	
25	cag	ggt	ctg	ggc	agc	cgg	gaa	gac	ctg	ctg	gca	gag	gtg	agt	ggg	ccc	6096
	Gln	Gly	Leu	Gly	Ser	Arg	Glu	Asp	Leu	Leu	Ala	Glu	Val	Ser	Gly	Pro	
						2020					2025					2030	
30	tcc	ccg	ccc	ctg	gcc	cgg	gcc	tac	tct	ttc	tgg	ggc	cag	tca	agt	acc	6144
	Ser	Pro	Pro	Leu	Ala	Arg	Ala	Tyr	Ser	Phe	Trp	Gly	Gln	Ser	Ser	Thr	
						2035					2040					2045	
35	cag	gca	cag	cag	cac	tcc	cgc	agc	cac	agc	aag	atc	tcc	aag	cac	atg	6192
	Gln	Ala	Gln	Gln	His	Ser	Arg	Ser	His	Ser	Lys	Ile	Ser	Lys	His	Met	
						2050					2055					2060	
	acc	ccg	cca	gcc	cct	tgc	cca	ggc	cca	gaa	ccc	aac	tgg	ggc	aag	ggc	6240
	Thr	Pro	Pro	Ala	Pro	Cys	Pro	Gly	Pro	Glu	Pro	Asn	Trp	Gly	Lys	Gly	
						2065						2075				2080	
40	cct	cca	gag	acc	aga	agc	agc	tta	gag	ttg	gac	acg	gag	ctg	agc	tgg	6288
	Pro	Pro	Glu	Thr	Arg	Ser	Ser	Leu	Glu	Leu	Asp	Thr	Glu	Leu	Ser	Trp	
						2085					2090					2095	
45	att	tca	gga	gac	ctc	ctg	ccc	cct	ggc	ggc	cag	gag	gag	ccc	cca	tcc	6336
	Ile	Ser	Gly	Asp	Leu	Leu	Pro	Pro	Gly	Gly	Gln	Glu	Glu	Pro	Pro	Ser	
						2100					2105					2110	
50	cca	cgg	gac	ctg	aag	aag	tgc	tac	agc	gtg	gag	gcc	cag	agc	tgc	cag	6384
	Pro	Arg	Asp	Leu	Lys	Lys	Cys	Tyr	Ser	Val	Glu	Ala	Gln	Ser	Cys	Gln	
						2115					2120					2125	
55	cgc	cgg	cct	acg	tcc	tgg	ctg	gat	gag	cag	agg	aga	cac	tct	atc	gcc	6432
	Arg	Arg	Pro	Thr	Ser	Trp	Leu	Asp	Glu	Gln	Arg	Arg	His	Ser	Ile	Ala	
						2130					2135					2140	
	gtc	agc	tgc	ctg	gac	agc	ggc	tcc	caa	ccc	cac	ctg	ggc	aca	gac	ccc	6480
	Val	Ser	Cys	Leu	Asp	Ser	Gly	Ser	Gln	Pro	His	Leu	Gly	Thr	Asp	Pro	
						2145					2155					2160	
60	tct	aac	ctt	ggg	ggc	cag	cct	ctt	ggg	ggg	cct	ggg	agc	cgg	ccc	aag	6528
	Ser	Asn	Leu	Gly	Gly	Gln	Pro	Leu	Gly	Gly	Pro	Gly	Ser	Arg	Pro	Lys	
						2165					2170					2175	
	aaa	aaa	ctc	agc	ccg	cct	agt	atc	acc	ata	gac	ccc	ccc	gag	agc	caa	6576

	Lys	Lys	Leu	Ser	Pro	Pro	Ser	Ile	Thr	Ile	Asp	Pro	Pro	Glu	Ser	Gln	
				2180					2185					2190			
5	ggt	cct	cgg	acc	ccg	ccc	aga	ccg	ggt	atc	tgc	ctc	cgg	agg	agg	gct	6624
	Gly	Pro	Arg	Thr	Pro	Pro	Ser	Pro	Gly	Ile	Cys	Leu	Arg	Arg	Arg	Ala	
			2195				2200					2205					
10	ccg	tcc	agc	gac	tcc	aag	gat	ccc	ttg	gcc	tct	ggc	ccc	cct	gac	agc	6672
	Pro	Ser	Ser	Asp	Ser	Lys	Asp	Pro	Leu	Ala	Ser	Gly	Pro	Pro	Asp	Ser	
		2210				2215					2220						
15	atg	gct	gcc	tcg	ccc	tcc	cca	aag	aaa	gat	gtg	ctg	agt	ctc	tcc	ggt	6720
	Met	Ala	Ala	Ser	Pro	Ser	Pro	Lys	Lys	Asp	Val	Leu	Ser	Leu	Ser	Gly	
	2225				2230					2235					2240		
	tta	tcc	tct	gac	cca	gca	gac	ctg	gac	ccc							6750
	Leu	Ser	Ser	Asp	Pro	Ala	Asp	Leu	Asp	Pro							
				2245					2250								
20	<210> 2																
	<211> 6783																
	<212> DNA																
25	<213> Homo sapiens																
	<220>																
	<221> CDS																
	<222> (1)..(6783)																
30	<400> 2																
	atg	gac	gag	gag	gag	gat	gga	gcg	ggc	gcc	gag	gag	tcg	gga	cag	ccc	48
	Met	Asp	Glu	Glu	Glu	Asp	Gly	Ala	Gly	Ala	Glu	Glu	Ser	Gly	Gln	Pro	
	1				5				10					15			
35	cgg	agc	ttc	atg	cgg	ctc	aac	gac	ctg	tcg	ggg	gcc	ggg	ggg	cgg	ccg	96
	Arg	Ser	Phe	Met	Arg	Leu	Asn	Asp	Leu	Ser	Gly	Ala	Gly	Gly	Arg	Pro	
				20				25					30				
40	ggg	ccg	ggg	tca	gca	gaa	aag	gac	ccg	ggc	agc	gcg	gac	tcc	gag	gcg	144
	Gly	Pro	Gly	Ser	Ala	Glu	Lys	Asp	Pro	Gly	Ser	Ala	Asp	Ser	Glu	Ala	
			35				40					45					
45	gag	ggg	ctg	ccg	tac	ccg	gcg	ctg	gcc	ccg	gtg	gtt	ttc	ttc	tac	ttg	192
	Glu	Gly	Leu	Pro	Tyr	Pro	Ala	Leu	Ala	Pro	Val	Val	Phe	Phe	Tyr	Leu	
		50				55					60						
50	agc	cag	gac	agc	cgc	ccg	cgg	agc	tgg	tgt	ctc	cgc	acg	gtc	tgt	aac	240
	Ser	Gln	Asp	Ser	Arg	Pro	Arg	Ser	Trp	Cys	Leu	Arg	Thr	Val	Cys	Asn	
	65				70				75				80				
	ccc	tgg	ttt	gag	cgc	atc	agc	atg	ttg	gtc	atc	ctt	ctc	aac	tgc	gtg	288
	Pro	Trp	Phe	Glu	Arg	Ile	Ser	Met	Leu	Val	Ile	Leu	Leu	Asn	Cys	Val	
					85				90					95			
55	acc	ctg	ggc	atg	ttc	cgg	cca	tgc	gag	gac	atc	gcc	tgt	gac	tcc	cag	336
	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Ile	Ala	Cys	Asp	Ser	Gln	
				100				105					110				
60	cgc	tgc	cgg	atc	ctg	cag	gcc	ttt	gat	gac	ttc	atc	ttt	gcc	ttc	ttt	384
	Arg	Cys	Arg	Ile	Leu	Gln	Ala	Phe	Asp	Asp	Phe	Ile	Phe	Ala	Phe	Phe	
			115				120						125				
	gcc	gtg	gag	atg	gtg	gtg	aag	atg	gtg	gcc	ttg	ggc	atc	ttt	ggg	aaa	432
	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	

	130	135	140	
5	aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val 145 150 155 160	480		
10	atc gca ggg atg ctg gag tac tgg ctg gac ctg cag aac gtc agc ttc Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe 165 170 175	528		
15	tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn 180 185 190	576		
20	cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu 195 200 205	624		
25	ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile 210 215 220	672		
30	ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg 225 230 235 240	720		
35	tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu 245 250 255	768		
40	cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser 260 265 270	816		
45	cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu 275 280 285	864		
50	cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala 290 295 300	912		
55	tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr 305 310 315 320	960		
60	acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn 325 330 335	1008		
65	ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr 340 345 350	1056		
70	ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser 355 360 365	1104		
75	ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe 370 375 380	1152		
80	ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu 385 390 395	1200		

	385		390		395		400	
5	acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc	1246						
	Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe		405	410	415			
10	ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc	1296						
	Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys		420	425	430			
15	tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc	1344						
	Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala		435	440	445			
20	cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg	1392						
	Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu		450	455	460			
25	ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc	1440						
	Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser		465	470	475			480
30	agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac	1488						
	Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His		485	490	495			
35	cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc	1536						
	His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu		500	505	510			
40	agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg	1584						
	Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly		515	520	525			
45	tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg	1632						
	Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly		530	535	540			
50	gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac	1680						
	Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp		545	550	555			560
55	tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca	1728						
	Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro		565	570	575			
60	tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc	1776						
	Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr		580	585	590			
65	gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta	1824						
	Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val		595	600	605			
70	gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc	1872						
	Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile		610	615	620			
75	cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt	1920						
	Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser		625	630	635			640
80	aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa	1968						
	Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys							

	645	650	655	
5	gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg 660 665 670	2016		
10	gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser 675 680 685	2064		
15	gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp 690 695 700	2112		
20	ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala 705 710 715 720	2160		
25	gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe 725 730 735	2208		
30	cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala 740 745 750	2256		
35	atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro 755 760 765	2304		
40	gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser 770 775 780	2352		
45	ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe 785 790 795 800	2400		
50	ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val 805 810 815	2448		
55	atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val 820 825 830	2496		
60	ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu 835 840 845	2544		
65	ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn 850 855 860	2592		
70	gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser 865 870 875 880	2640		
75	atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp 885 890 895	2688		
80	ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala 900 905 910 915	2736		

	900						905						910						
5	atc	gtc	act	gtc	ttt	cag	atc	ctg	acc	cag	gag	gac	tgg	aac	aaa	gtc	2784		
	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Lys	Val			
			915					920					925						
10	ctc	tac	aat	ggt	atg	gcc	tcc	acg	tcg	tcc	tgg	gcg	gcc	ctt	tat	ttc	2832		
	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr	Phe			
			930				935					940							
15	att	gcc	ctc	atg	acc	ttc	ggc	aac	tac	gtg	ctc	ttc	aat	ttg	ctg	gtc	2880		
	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	Val			
			945			950					955					960			
20	gaa	tca	gag	ccc	gat	ttc	ttc	tca	ccc	agc	ctg	gat	ggt	gat	ggg	gac	2976		
	Glu	Ser	Glu	Pro	Asp	Phe	Phe	Ser	Pro	Ser	Leu	Asp	Gly	Asp	Gly	Asp			
				980					985					990					
25	agg	aag	aag	tgc	ttg	gcc	ttg	gtg	tcc	ctg	gga	gag	cac	ccg	gag	ctg	3024		
	Arg	Lys	Lys	Cys	Leu	Ala	Leu	Val	Ser	Leu	Gly	Glu	His	Pro	Glu	Leu			
			995				1000						1005						
30	cgg	aag	agc	ctg	ctg	ccg	cct	ctc	atc	atc	cac	acg	gcc	gcc	aca	ccc	3072		
	Arg	Lys	Ser	Leu	Leu	Pro	Pro	Leu	Ile	Ile	His	Thr	Ala	Ala	Thr	Pro			
		1010					1015					1020							
35	atg	tcg	ctg	ccc	aag	agc	acc	agc	acg	ggc	ctg	ggc	gag	gcg	ctg	ggc	3120		
	Met	Ser	Leu	Pro	Lys	Ser	Thr	Ser	Thr	Gly	Leu	Gly	Glu	Ala	Leu	Gly			
					1025		1030				1035					1040			
40	cct	gcg	tcg	cgc	cgc	acc	agc	agc	agc	ggg	tcg	gca	gag	cct	ggg	gcg	3168		
	Pro	Ala	Ser	Arg	Arg	Thr	Ser	Ser	Ser	Gly	Ser	Ala	Glu	Pro	Gly	Ala			
					1045					1050					1055				
45	gcc	cac	gag	atg	aag	tca	ccg	ccc	agc	gcc	cgc	agc	tct	ccg	cac	agc	3216		
	Ala	His	Glu	Met	Lys	Ser	Pro	Pro	Ser	Ala	Arg	Ser	Ser	Pro	His	Ser			
				1060					1065					1070					
50	ccc	tgg	agc	gct	gca	agc	agc	tgg	acc	agc	agg	cgc	tcc	agc	cgg	aac	3264		
	Pro	Trp	Ser	Ala	Ala	Ser	Ser	Trp	Thr	Ser	Arg	Arg	Ser	Ser	Arg	Asn			
			1075					1080					1085						
55	agc	ctc	ggc	cgt	gca	ccc	agc	ctg	aag	cgg	aga	agc	cca	agt	gga	gag	3312		
	Ser	Leu	Gly	Arg	Ala	Pro	Ser	Leu	Lys	Arg	Arg	Ser	Pro	Ser	Gly	Glu			
		1090					1095					1100							
60	cgg	cgg	tcc	ctg	ttg	tcg	gga	gaa	ggc	cag	gag	agc	cag	gat	gaa	gag	3360		
	Arg	Arg	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gln	Glu	Ser	Gln	Asp	Glu	Glu			
						1110					1115					1120			
65	gag	agc	tca	gaa	gag	gag	cgg	gcc	agc	cct	gcg	ggc	agt	gac	cat	cgc	3408		
	Glu	Ser	Ser	Glu	Glu	Glu	Arg	Ala	Ser	Pro	Ala	Gly	Ser	Asp	His	Arg			
					1125					1130					1135				
70	cac	agg	ggg	tcc	ctg	gag	cgg	gag	gcc	aag	agt	tcc	ttt	gac	ctg	cca	3456		
	His	Arg	Gly	Ser	Leu	Glu	Arg	Glu	Ala	Lys	Ser	Ser	Phe	Asp	Leu	Pro			
				1140					1145					1150					
75	gac	aca	ctg	cag	gtg	cca	ggg	ctg	cat	cgc	act	gcc	agt	ggc	cga	ggg	3504		
	Asp	Thr	Leu	Gln	Val	Pro	Gly	Leu	His	Arg	Thr	Ala	Ser	Gly	Arg	Gly			



	1155	1160	1165	
5	tct gct tct gag cac cag gac tgc aat ggc aag tgc gct tca ggg cgc Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg 1170 1175 1180			3552
10	ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp 1185 1190 1195 1200			3600
15	gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp 1205 1210 1215			3648
20	atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser 1220 1225 1230			3696
25	gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg 1235 1240 1245			3744
30	atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe 1250 1255 1260			3792
35	ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His 1265 1270 1275 1280			3840
40	agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala 1285 1290 1295			3888
45	gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys 1300 1305 1310			3936
50	ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly 1315 1320 1325			3984
55	ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser 1330 1335 1340			4032
60	gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu 1345 1350 1355 1360			4080
65	cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys 1365 1370 1375			4128
70	ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile 1380 1385 1390			4176
75	gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val 1395 1400 1405			4224
80	cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg 1410 1415 1420 1425 1430 1435 1440 1445 1450			4272

	1410	1415	1420	
5	aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val 1425 1430 1435 1440	4320		
10	cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu 1445 1450 1455	4368		
	ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly 1460 1465 1470	4416		
15	ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro 1475 1480 1485	4464		
20	tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Val Ala Phe Phe 1490 1495 1500	4512		
25	gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys 1505 1510 1515 1520	4560		
30	cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg 1525 1530 1535	4608		
	cta cga aga ctg gag aaa aag aga agg aat cta atg ctg gac gat gta Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp Asp Val 1540 1545 1550	4656		
35	att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag tgc aaa Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln Cys Lys 1555 1560 1565	4704		
40	cct tac tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu 1570 1575 1580	4752		
45	tgc acc agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu 1585 1590 1595 1600	4800		
50	aac gtg gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu 1605 1610 1615	4848		
	gat gag gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val 1620 1625 1630	4896		
55	ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe 1635 1640 1645	4944		
60	cag gac agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile 1650 1655 1660	4992		
	atg gcc atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile	5040		

	1665	1670	1675	1680	
5	aac ccc acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val	1685	1690	1695	5088
10	ctg aag ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr	1700	1705	1710	5136
15	gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met	1715	1720	1725	5184
20	ttg ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp	1730	1735	1740	5232
25	ctg gag tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala	1745	1750	1755	5280
30	acc ttt cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser	1765	1770	1775	5328
35	aca ggt gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys	1780	1785	1790	5376
40	gac cag gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe	1795	1800	1805	5424
45	gtg tcc ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile	1810	1815	1820	5472
50	gcc gtg ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu	1825	1830	1835	5520
55	gag gcc gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser	1845	1850	1855	5568
60	ccc cag ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val	1860	1865	1870	5616
65	gag ggc ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro	1875	1880	1885	5664
70	gcg gcc cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg Ala Ala His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr	1890	1895	1900	5712
75	atg cag ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val	1905	1910	1915	5760
80	cgg aag tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr				5808

	1925	1930	1935	
5	atg tgt cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly 1940 1945 1950	5856		
10	tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser 1955 1960 1965	5904		
15	cag cca gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro 1970 1975 1980	5952		
20	cat ctg ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa His Leu Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys 1985 1990 2000	6000		
25	ctg ccc cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg 2005 2010 2015	6048		
30	cag gca gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser 2020 2025 2030	6096		
35	cgg gaa gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala 2035 2040 2045	6144		
40	cgg gcc tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His 2050 2055 2060	6192		
45	tcc cgc agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct Ser Arg Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro 2065 2070 2075 2080	6240		
50	tgc cca ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg 2085 2090 2095	6288		
55	agc agc tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu 2100 2105 2110	6336		
60	ctg ccc cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys 2115 2120 2125	6384		
65	aag tgc tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser 2130 2135 2140	6432		
70	tgg ctg gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp 2145 2150 2155 2160	6480		
75	agc ggc tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly 2165 2170 2175	6528		
80	cag cct ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro 2180 2185 2190 2195	6576		

	2190	2195	2200	2205	2210	2215	2220	2225	2230	2235	2240	2245	2250	2255	
5	cct agt atc acc ata gac ccc ccc gag agc caa ggt cct cgg acc cgg														6624
	Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro														
10	ccc agc cct ggt atc tgc ctc cgg agg agg gct cgg tcc agc gac tcc														6672
	Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser														
15	aag gat ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc														6720
	Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro														
20	tcc cca aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca														6768
	Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro														
25	gca gac ctg gac ccc														6783
	Ala Asp Leu Asp Pro														
30	<210> 3														
	<211> 6804														
	<212> DNA														
	<213> Homo sapiens														
35	<220>														
	<221> CDS														
	<222> (1)...(6804)														
40	<400> 3														
	atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc														48
	Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro														
45	cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg														96
	Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro														
50	ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg														144
	Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala														
55	gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg														192
	Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu														
60	agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac														240
	Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn														
65	ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg														288
	Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val														
70	acc ctg ggc atg ttc cgg oca tgc gag gac atc gcc tgt gac tcc cag														336
	Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln														
75	cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt														384
	Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe														

5	gcc	gtg	gag	atg	gtg	gtg	aag	atg	gtg	gcc	tgg	ggc	atc	ttt	ggg	aaa	432
	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	
	130						135					140					
10	aag	tgt	tac	ctg	gga	gac	act	tgg	aac	cgg	ctt	gac	att	ttc	atc	gtc	480
	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val	
	145					150					155					160	
15	atc	gca	ggg	atg	ctg	gag	tac	tgg	ctg	gac	ctg	cag	aac	gtc	agc	ttc	528
	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe	
					165					170					175		
20	tca	gct	gtc	agg	aca	gtc	cgt	gtg	ctg	cga	cgg	ctc	agg	gcc	att	aac	576
	Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn	
				180					185					190			
25	cgg	gtg	ccc	agc	atg	cgc	atc	ctt	gtc	acg	tgg	ctg	ctg	gat	acg	ctg	624
	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu	
			195					200					205				
30	ccc	atg	ctg	ggc	aac	gtc	ctg	ctg	ctc	tgc	ttc	ttc	gtc	ttc	ttc	atc	672
	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	
		210					215					220					
35	ttc	ggc	atc	gtc	ggc	gtc	cag	ctg	tgg	gca	ggg	ctg	ctt	cgg	aac	cga	720
	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	
	225				230					235						240	
40	tgc	ttc	cta	cct	gag	aat	ttc	agc	ctc	ccc	ctg	agc	gtg	gac	ctg	gag	768
	Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu	
					245					250					255		
45	cgc	tat	tac	cag	aca	gag	aac	gag	gat	gag	agc	ccc	ttc	atc	tgc	tcc	816
	Arg	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser	
				260					265					270			
50	cag	cca	cgc	gag	aac	ggc	atg	cgg	tcc	tgc	aga	agc	gtg	ccc	acg	ctg	864
	Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu	
			275					280					285				
55	cgc	ggg	gac	ggg	ggc	ggt	ggc	cca	cct	tgc	ggt	ctg	gac	tat	gag	gcc	912
	Arg	Gly	Asp	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Gly	Leu	Asp	Tyr	Glu	Ala	
		290				295						300					
60	tac	aac	agc	tcc	agc	aac	acc	acc	tgt	gtc	aac	tgg	aac	cag	tac	tac	960
	Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr	
	305					310					315					320	
65	acc	aac	tgc	tca	gcg	ggg	gag	cac	aac	ccc	ttc	aag	ggc	gcc	atc	aac	1008
	Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn	
					325					330					335		
70	ttt	gac	aac	att	ggc	tat	gcc	tgg	atc	gcc	atc	ttc	cag	gtc	atc	acg	1056
	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr	
				340				345						350			
75	ctg	gag	ggc	tgg	gtc	gac	atc	atg	tac	ttt	gtg	atg	gat	gct	cat	tcc	1104
	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser	
			355					360					365				
80	ttc	tac	aat	ttc	atc	tac	ttc	atc	ctc	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
	370						375					380					

5	ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag	1200
	Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu	
	385 390 395 400	
10	acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc	1248
	Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe	
	405 410 415	
15	ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc	1296
	Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys	
	420 425 430	
20	tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc	1344
	Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala	
	435 440 445	
25	cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg ggt ggg ctg	1392
	Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu	
	450 455 460	
30	ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc	1440
	Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser	
	465 470 475 480	
35	agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac	1488
	Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His	
	485 490 495	
40	cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc	1536
	His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu	
	500 505 510	
45	agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg	1584
	Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly	
	515 520 525	
50	tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg	1632
	Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly	
	530 535 540	
55	gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac	1680
	Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp	
	545 550 555 560	
60	tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca	1728
	Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro	
	565 570 575	
65	tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc	1776
	Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr	
	580 585 590	
70	gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta	1824
	Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val	
	595 600 605	
75	gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc	1872
	Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile	
	610 615 620	
80	cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt	1920
	Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser	
	625 630 635 640	

	aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc tgg aaa	1968
	Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys	
	645 650 655	
5	gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg	2016
	Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg	
	660 665 670	
10	gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca	2064
	Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser	
	675 680 685	
15	gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac	2112
	Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp	
	690 695 700	
20	ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca	2160
	Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala	
	705 710 715 720	
25	gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc	2208
	Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe	
	725 730 735	
30	cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc	2256
	Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala	
	740 745 750	
35	atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc	2304
	Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro	
	755 760 765	
40	gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc	2352
	Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser	
	770 775 780	
45	ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt	2400
	Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe	
	785 790 795 800	
50	ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc	2448
	Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val	
	805 810 815	
55	atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tgc gtg	2496
	Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val	
	820 825 830	
60	ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg	2544
	Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu	
	835 840 845	
65	ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac	2592
	Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn	
	850 855 860	
70	gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc	2640
	Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser	
	865 870 875 880	
75	atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat	2688
	Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp	
	885 890 895	



	ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc	2736
	Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala	
	900 905 910	
5	atc gtc acc gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc	2784
	Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val	
	915 920 925	
10	ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc	2832
	Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe	
	930 935 940	
15	att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc	2880
	Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val	
	945 950 955 960	
20	gcc att ctg gtg gag gcc ttc cag gcg gag gga gat gcc aac aag tcc	2928
	Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser	
	965 970 975	
25	gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac	2976
	Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp	
	980 985 990	
30	agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg	3024
	Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu	
	995 1000 1005	
35	cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc	3072
	Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro	
	1010 1015 1020	
40	atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc	3120
	Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly	
	1025 1030 1035 1040	
45	cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg	3168
	Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala	
	1045 1050 1055	
50	gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc	3216
	Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser	
	1060 1065 1070	
55	ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac	3264
	Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn	
	1075 1080 1085	
60	agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag	3312
	Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu	
	1090 1095 1100	
65	cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag	3360
	Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu	
	1105 1110 1115 1120	
70	gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc	3408
	Glu Ser Ser Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg	
	1125 1130 1135	
75	cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca	3456
	His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro	
	1140 1145 1150	

gac aca ctg cag gtg cca ggg ctg cat cgg act gcc agt ggc cga ggg 3504  
 Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly  
 1155 1160 1165

5 tct gct tct gag cac cag gac tgc aat ggc aag tgg gct tca ggg cgc 3552  
 Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg  
 1170 1175 1180

10 ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac 3600  
 Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp  
 1185 1190 1195 1200

15 gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg 3648  
 Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp  
 1205 1210 1215

20 atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca 3696  
 Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser  
 1220 1225 1230

25 gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg 3744  
 Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg  
 1235 1240 1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc 3792  
 Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe  
 1250 1255 1260

30 ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac 3840  
 Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His  
 1265 1270 1275 1280

35 agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca 3888  
 Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala  
 1285 1290 1295

40 gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc 3936  
 Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys  
 1300 1305 1310

45 ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg 3984  
 Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly  
 1315 1320 1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct 4032  
 Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser  
 1330 1335 1340

50 gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg 4080  
 Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu  
 1345 1350 1355 1360

55 cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag 4128  
 Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys  
 1365 1370 1375

60 ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att 4176  
 Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile  
 1380 1385 1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg 4224  
 Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val  
 1395 1400 1405

5 cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg 4272  
 Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg  
 1410 1415 1420  
 aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc 4320  
 Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val  
 1425 1430 1435 1440  
 10 cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg 4368  
 Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu  
 1445 1450 1455  
 15 ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg 4416  
 Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly  
 1460 1465 1470  
 20 ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc 4464  
 Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro  
 1475 1480 1485  
 tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt 4512  
 Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe  
 1490 1495 1500  
 25 gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt 4560  
 Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys  
 1505 1510 1515 1520  
 30 cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc 4608  
 Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg  
 1525 1530 1535  
 35 cta cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct 4656  
 Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala  
 1540 1545 1550  
 40 gat cta atg ctg gac gat gta att gct tcc ggc agc tca gcc agc gct 4704  
 Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala  
 1555 1560 1565  
 45 gcg tca gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc 4752  
 Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe  
 1570 1575 1580  
 cgg ctc ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc 4800  
 Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe  
 1585 1590 1595 1600  
 50 atc aca ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac 4848  
 Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His  
 1605 1610 1615  
 55 tac cag cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac 4896  
 Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr  
 1620 1625 1630  
 60 atc ttc act gtc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc 4944  
 Ile Phe Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala  
 1635 1640 1645  
 ttt ggt ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg 4992  
 Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu  
 1650 1655 1660

5	gcc att gtg ctg ctg tcc atc atg ggc atc acg ctg gag gaa atc gag	5040
	Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu	
	1665 1670 1675 1680	
10	gtc aac gcc tgc ctg ccc atc aac ccc acc atc atc cgc atc atg agg	5088
	Val Asn Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg	
	1685 1690 1695	
15	gtg ctg cgc att gcc cga gtg ctg aag ctg ctg aag atg gct gtg ggc	5136
	Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly	
	1700 1705 1710	
20	atg cgg gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg	5184
	Met Arg Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly	
	1715 1720 1725	
25	aac ctg gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gct ctg	5232
	Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu	
	1730 1735 1740	
30	ggc gtg gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt	5280
	Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys	
	1745 1750 1755 1760	
35	gag ggc ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc	5328
	Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe	
	1765 1770 1775	
40	cta acc ctc ttc cga gtc tcc aca ggt gac aat tgg aat ggc att atg	5376
	Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met	
	1780 1785 1790	
45	aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg	5424
	Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr	
	1795 1800 1805	
50	gtc atc tgc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttc	5472
	Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe	
	1810 1815 1820	
55	gtg cta gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag	5520
	Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu	
	1825 1830 1835 1840	
60	agc aac aag gag gcc aag gag gag gcc gag cta gag gct gag ctg gag	5568
	Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu	
	1845 1850 1855	
65	ctg gag atg aag acc ctc agc ccc cag ccc cac tgc cca ctg ggc agc	5616
	Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser	
	1860 1865 1870	
70	ccc ttc ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc	5664
	Pro Phe Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro	
	1875 1880 1885	
75	aag cct ggg gct ctg cac cca gcg gcc cac gcg aga tca gcc tcc cac	5712
	Lys Pro Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His	
	1890 1895 1900	
80	ttt tcc ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca	5760
	Phe Ser Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro	
	1905 1910 1915 1920	

	gga cca gac tta ctg act gtg cgg aag tct ggg gtc agc cga acg cac	5808
	Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His	
	1925 1930 1935	
5	tct ctg ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag	5856
	Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu	
	1940 1945 1950	
10	ggg ccc ctg gga cac agg ggc tgg ggg ctc ccc aaa gct cag tca ggc	5904
	Gly Pro Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly	
	1955 1960 1965	
15	tcc gtc ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg	5952
	Ser Val Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu	
	1970 1975 1980	
20	cag ctt ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca	6000
	Gln Leu Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro	
	1985 1990 1995 2000	
25	acc tgg ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg	6048
	Thr Trp Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu	
	2005 2010 2015	
30	gct cag agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg	6096
	Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu	
	2020 2025 2030	
35	gac gtt cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt	6144
	Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser	
	2035 2040 2045	
40	ggg ccc tcc ccg ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca	6192
	Gly Pro Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser	
	2050 2055 2060	
45	agt acc cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag	6240
	Ser Thr Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys	
	2065 2070 2075 2080	
50	cac atg acc ccg cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc	6288
	His Met Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly	
	2085 2090 2095	
55	aag ggc cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg	6336
	Lys Gly Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu	
	2100 2105 2110	
60	agc tgg att tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc	6384
	Ser Trp Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro	
	2115 2120 2125	
65	cca tcc cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc	6432
	Pro Ser Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser	
	2130 2135 2140	
70	tgc cag cgc cgg cct acg tcc tgg ctg gat gag cag agg aga cac tct	6480
	Cys Gln Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser	
	2145 2150 2155 2160	
75	atc gcc gtc agc tgc ctg gac agc ggc tcc caa ccc cac ctg ggc aca	6528
	Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr	
	2165 2170 2175	

5 gac ccc tct aac ctt ggg ggc cag cct ctt ggg ggg cct ggg agc cgg 6576  
 Asp Pro Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg  
 2180 2185 2190

10 ccc aag aaa aaa ctc agc cgg cct agt atc acc ata gac ccc ccc gag 6624  
 Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu  
 2195 2200 2205

15 agc caa ggt cct cgg acc cgg ccc agc cct ggt atc tgc ctc cgg agg 6672  
 Ser Gln Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg  
 2210 2215 2220

20 agg gct ccg tcc agc gac tcc aag gat ccc ttg gcc tct ggc ccc cct 6720  
 Arg Ala Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro  
 2225 2230 2235 2240

25 gac agc atg gct gcc tcg ccc tcc cca aag aaa gat gtg ctg agt ctc 6768  
 Asp Ser Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu  
 2245 2250 2255

30 tcc ggt tta tcc tct gac cca gca gac ctg gac ccc 6804  
 Ser Gly Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro  
 2260 2265

35 <210> 4  
 <211> 6729  
 <212> DNA  
 <213> Homo sapiens

40 <220>  
 <221> CDS  
 <222> (1)..(6729)

45 <400> 4  
 atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc 48  
 Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro  
 1 5 10 15

50 cgg agc ttc atg cgg ctc aac gac ctg tcg ggg gcc ggg ggg cgg ccg 96  
 Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro  
 20 25 30

55 ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144  
 Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala  
 35 40 45

60 gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg 192  
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu  
 50 55 60

65 agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240  
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn  
 65 70 75 80

70 ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg 288  
 Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val  
 85 90 95

75 acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag 336  
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln  
 100 105 110

	cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt	384
	Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe	
	115 120 125	
5	gcc gtg gag atg gtg gtg aag atg gtg gcc ttg gcc atc ttt ggg aaa	432
	Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys	
	130 135 140	
10	aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc	480
	Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val	
	145 150 155 160	
15	atc gca ggg atg ctg gag tac tgg ctg gac ctg cag aac gtc agc ttc	528
	Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe	
	165 170 175	
20	tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac	576
	Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn	
	180 185 190	
25	cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg	624
	Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu	
	195 200 205	
30	ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc	672
	Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile	
	210 215 220	
35	ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga	720
	Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg	
	225 230 235 240	
40	tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag	768
	Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu	
	245 250 255	
45	cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc	816
	Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser	
	260 265 270	
50	cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg	864
	Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu	
	275 280 285	
55	cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc	912
	Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala	
	290 295 300	
60	tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac	960
	Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr	
	305 310 315 320	
65	acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac	1008
	Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn	
	325 330 335	
70	ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg	1056
	Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr	
	340 345 350	
75	ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc	1104
	Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser	
	355 360 365	

	ttc	tac	aat	ttc	atc	tac	ttc	atc	ctc	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
	370						375					380					
5	ttc	atg	atc	aac	ctg	tgc	ctg	gtg	gtg	att	gcc	acg	cag	ttc	tca	gag	1200
	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu	
	385					390					395					400	
10	acc	aag	cag	ggg	gaa	agc	cag	ctg	atg	cgg	gag	cag	cgt	gtg	egg	ttc	1248
	Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe	
					405					410					415		
15	ctg	tcc	aac	gcc	agc	acc	ctg	gct	agc	ttc	tct	gag	ccc	ggc	agg	tgc	1296
	Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys	
				420					425					430			
20	tat	gag	gag	ctg	ctc	aag	tac	ctg	gtg	tac	atc	ctt	cgt	aag	gca	gcc	1344
	Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala	
				435				440					445				
25	cgc	agg	ctg	gct	cag	gtc	tct	cgg	gca	gca	ggg	gtg	cgg	gtt	ggg	ctg	1392
	Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ala	Gly	Val	Arg	Val	Gly	Leu	
	450						455					460					
30	ctc	agc	agc	cca	gca	ccc	ctc	ggg	ggc	cag	gag	acc	cag	ccc	agg	agc	1440
	Leu	Ser	Ser	Pro	Ala	Pro	Leu	Gly	Gly	Gln	Glu	Thr	Gln	Pro	Ser	Ser	
	465					470					475					480	
35	agc	tgc	tct	cgc	tcc	cac	cgc	cgc	cta	tcc	gtc	cac	cac	ctg	gtg	cac	1488
	Ser	Cys	Ser	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His	
					485					490					495		
40	cac	cac	cac	cac	cat	cac	cac	cac	tac	cac	ctg	ggc	aat	ggg	acg	ctc	1536
	His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu	
				500					505					510			
45	agg	gcc	ccc	cgg	gcc	agc	ccg	gag	atc	cag	gac	agg	gat	gcc	aat	ggg	1584
	Arg	Ala	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly	
				515				520					525				
50	tcc	cgc	cgg	ctc	atg	ctg	cca	cca	ccc	tcg	acg	cct	gcc	ctc	tcc	ggg	1632
	Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr	Pro	Ala	Leu	Ser	Gly	
	530						535					540					
55	gcc	ccc	cct	ggg	ggc	gca	gag	tct	gtg	cac	agc	ttc	tac	cat	gcc	gac	1680
	Ala	Pro	Pro	Gly	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp	
	545					550					555					560	
60	tgc	cac	tta	gag	cca	gtc	cgc	tgc	cag	gcg	ccc	cct	ccc	agg	tcc	cca	1728
	Cys	His	Leu	Glu	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Ser	Pro	
					565					570					575		
65	tct	gag	gca	tcc	ggc	agg	act	gtg	ggc	agc	ggg	aag	gtg	tat	ccc	acc	1776
	Ser	Glu	Ala	Ser	Gly	Arg	Thr	Val	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr	
				580					585					590			
70	gtg	cac	acc	agc	cct	cca	ccg	gag	acg	ctg	aag	gag	aag	gca	cta	gta	1824
	Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Thr	Leu	Lys	Glu	Lys	Ala	Leu	Val	
			595					600					605				
75	gag	gtg	gct	gcc	agc	tct	ggg	ccc	cca	acc	ctc	acc	agc	ctc	aac	atc	1872
	Glu	Val	Ala	Ala	Ser	Ser	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Leu	Asn	Ile	
	610						615					620					



	cca	ccc	ggg	ccc	tac	agc	tcc	atg	cac	aag	ctg	ctg	gag	aca	cag	agt	1920
	Pro	Pro	Gly	Pro	Tyr	Ser	Ser	Met	His	Lys	Leu	Leu	Glu	Thr	Gln	Ser	
	625					630					635					640	
5	aca	ggt	gcc	tgc	caa	agc	tct	tgc	aag	atc	tcc	agc	cct	tgc	ttg	aaa	1968
	Thr	Gly	Ala	Cys	Gln	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Leu	Lys	
					645					650					655		
10	gca	gac	agt	gga	gcc	tgt	ggt	cca	gac	agc	tgc	ccc	tac	tgt	gcc	cgg	2016
	Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pro	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg	
				660					665					670			
15	gcc	ggg	gca	ggg	gag	gtg	gag	ctc	gcc	gac	cgt	gaa	atg	cct	gac	tca	2064
	Ala	Gly	Ala	Gly	Glu	Val	Glu	Leu	Ala	Asp	Arg	Glu	Met	Pro	Asp	Ser	
			675					680					685				
20	gac	agc	gag	gca	gtt	tat	gag	ttc	aca	cag	gat	gcc	cag	cac	agc	gac	2112
	Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp	
		690					695					700					
25	ctc	cgg	gac	ccc	cac	agc	cgg	cgg	caa	cgg	agc	ctg	ggc	cca	gat	gca	2160
	Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	Ala	
	705					710					715					720	
30	gag	ccc	agc	tct	gtg	ctg	gcc	ttc	tgg	agg	cta	atc	tgt	gac	acc	ttc	2208
	Glu	Pro	Ser	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	Phe	
					725				730						735		
35	cga	aag	att	gtg	gac	agc	aag	tac	ttt	ggc	cgg	gga	atc	atg	atc	gcc	2256
	Arg	Lys	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	Ala	
				740					745					750			
40	atc	ctg	gtc	aac	aca	ctc	agc	atg	ggc	atc	gaa	tac	cac	gag	cag	ccc	2304
	Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	Glu	Tyr	His	Glu	Gln	Pro	
			755					760					765				
45	gag	gag	ctt	acc	aac	gcc	cta	gaa	atc	agc	aac	atc	gtc	ttc	acc	agc	2352
	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr	Ser	
		770					775					780					
50	ctc	ttt	gcc	ctg	gag	atg	ctg	ctg	aag	ctg	ctt	gtg	tat	ggt	ccc	ttt	2400
	Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	Phe	
	785					790					795					800	
55	ggc	tac	atc	aag	aat	ccc	tac	aac	atc	ttc	gat	ggt	gtc	att	gtg	gtc	2448
	Gly	Tyr	Ile	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	Val	
					805				810					815			
60	atc	agc	gtg	tgg	gag	atc	gtg	ggc	cag	cag	ggg	ggc	ggc	ctg	tgg	gtg	2496
	Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser	Val	
				820				825						830			
65	ctg	cgg	acc	ttc	cgc	ctg	atg	cgt	gtg	ctg	aag	ctg	gtg	cgc	ttc	ctg	2544
	Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	Leu	
			835					840					845				
70	ccg	gcg	ctg	cag	cgg	cag	ctg	gtg	gtg	ctc	atg	aag	acc	atg	gac	aac	2592
	Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	Asn	
		850					855					860					
75	gtg	gcc	acc	ttc	tgc	atg	ctg	ctt	atg	ctc	ttc	atc	ttc	atc	ttc	agc	2640
	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	Ser	
	865					870					875					880	

	atc	ctg	ggc	atg	cat	ctc	ttc	ggc	tgc	aag	ttt	gcc	tct	gag	cgg	gat	2633
	Ile	Leu	Gly	Met	His	Leu	Phe	Gly	Cys	Lys	Phe	Ala	Ser	Glu	Arg	Asp	
				285						390					895		
5	ggg	gac	acc	ctg	cca	gac	cgg	aag	aat	ttt	gac	tcc	ttg	ctc	tgg	gcc	2736
	Gly	Asp	Thr	Leu	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp	Ala	
				900					905					910			
10	atc	gtc	act	gtc	ttc	cag	atc	ctg	acc	cag	gag	gac	tgg	aac	aaa	gtc	2784
	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Lys	Val	
				915				920					925				
15	ctc	tac	aat	ggt	atg	gcc	tcc	acg	tgc	tcc	tgg	gcg	gcc	cct	tat	ttc	2832
	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr	Phe	
				930			935					940					
20	att	gcc	ctc	atg	acc	ttc	ggc	aac	tac	gtg	ctc	ttc	aat	ttg	ctg	gtc	2880
	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	Val	
						950					955					960	
	gcc	att	ctg	gtg	gag	ggc	ttc	cag	gcg	gag	gga	gat	gcc	aac	aag	tcc	2928
	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Gly	Asp	Ala	Asn	Lys	Ser	
					965					970					975		
25	gaa	tca	gag	ccc	gat	ttc	ttc	tca	ccc	agc	ctg	gat	ggt	gat	ggg	gac	2976
	Glu	Ser	Glu	Pro	Asp	Phe	Phe	Ser	Pro	Ser	Leu	Asp	Gly	Asp	Gly	Asp	
				980					985					990			
30	agg	aag	aag	tgc	ttg	gcc	ttg	gtg	tcc	ctg	gga	gag	cac	cgg	gag	ctg	3024
	Arg	Lys	Lys	Cys	Leu	Ala	Leu	Val	Ser	Leu	Gly	Glu	His	Pro	Glu	Leu	
			995				1000						1005				
35	cgg	aag	agc	ctg	ctg	cgg	cct	ctc	atc	atc	cac	acg	gcc	gcc	aca	ccc	3072
	Arg	Lys	Ser	Leu	Leu	Pro	Pro	Leu	Ile	Ile	His	Thr	Ala	Ala	Thr	Pro	
		1010				1015						1020					
40	atg	tgc	ctg	ccc	aag	agc	acc	agc	acg	ggc	ctg	ggc	gag	gcg	ctg	ggc	3120
	Met	Ser	Leu	Pro	Lys	Ser	Thr	Ser	Thr	Gly	Leu	Gly	Glu	Ala	Leu	Gly	
		1025			1030					1035					1040		
	cct	gcg	tgc	cgc	cgc	acc	agc	agc	agc	ggg	tgc	gca	gag	cct	ggg	gcg	3168
	Pro	Ala	Ser	Arg	Arg	Thr	Ser	Ser	Ser	Gly	Ser	Ala	Glu	Pro	Gly	Ala	
				1045						1050					1055		
45	gcc	cac	gag	atg	aag	tca	cgg	ccc	agc	gcc	cgc	agc	tct	cgg	cac	agc	3216
	Ala	His	Glu	Met	Lys	Ser	Pro	Pro	Ser	Ala	Arg	Ser	Ser	Pro	His	Ser	
				1060				1065						1070			
50	ccc	tgg	agc	gct	gca	agc	agc	tgg	acc	agc	agg	cgc	tcc	agc	cgg	aac	3264
	Pro	Trp	Ser	Ala	Ala	Ser	Ser	Trp	Thr	Ser	Arg	Arg	Ser	Ser	Arg	Asn	
		1075					1080						1085				
55	agc	ctc	ggc	cgt	gca	ccc	agc	ctg	aag	cgg	aga	agc	cca	agt	gga	gag	3312
	Ser	Leu	Gly	Arg	Ala	Pro	Ser	Leu	Lys	Arg	Arg	Ser	Pro	Ser	Gly	Glu	
		1090				1095					1100						
60	cgg	cgg	tcc	ctg	ttg	tgc	gga	gaa	ggc	cag	gag	agc	cag	gat	gaa	gag	3360
	Arg	Arg	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gln	Glu	Ser	Gln	Asp	Glu	Glu	
		1105			1110					1115					1120		
	gag	agc	tca	gaa	gag	gag	cgg	gcc	agc	cct	gcg	ggc	agt	gac	cat	cgc	3408
	Glu	Ser	Ser	Glu	Glu	Glu	Arg	Ala	Ser	Pro	Ala	Gly	Ser	Asp	His	Arg	
				1125				1130							1135		

	cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca	3456
	His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro	
	1140 1145 1150	
5	gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg	3504
	Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly	
	1155 1160 1165	
10	tct gct tct gag cac cag gac tgc aat ggc aag tgc gct tca ggg cgc	3552
	Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg	
	1170 1175 1180	
15	ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac	3600
	Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp	
	1185 1190 1195 1200	
20	gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc ggg tgg	3648
	Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp	
	1205 1210 1215	
25	atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca	3696
	Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser	
	1220 1225 1230	
30	gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg	3744
	Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg	
	1235 1240 1245	
35	atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc	3792
	Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe	
	1250 1255 1260	
40	ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac	3840
	Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His	
	1265 1270 1275 1280	
45	agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca	3888
	Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala	
	1285 1290 1295	
50	gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg gcc tgg tgc	3936
	Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys	
	1300 1305 1310	
55	ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg	3984
	Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly	
	1315 1320 1325	
60	ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct	4032
	Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser	
	1330 1335 1340	
65	gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg	4080
	Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu	
	1345 1350 1355 1360	
70	cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag	4128
	Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys	
	1365 1370 1375	
75	ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc gcc aac att	4176
	Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile	
	1380 1385 1390	

	gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg	4224
	Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val	
	1395 1400 1405	
5	cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg	4272
	Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg	
	1410 1415 1420	
10	aac atc acc aat aaa tgc gac tgt gcc gag gcc agt tac cgg tgg gtc	4320
	Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val	
	1425 1430 1435 1440	
15	cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg	4368
	Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu	
	1445 1450 1455	
20	ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg	4416
	Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly	
	1460 1465 1470	
25	ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc	4464
	Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro	
	1475 1480 1485	
30	tgg atg ctg ctg tac ttc atc tgc ttc ctg ctc att gtg gcc ttc ttt	4512
	Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe	
	1490 1495 1500	
35	gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt	4560
	Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys	
	1505 1510 1515 1520	
40	cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc	4608
	Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg	
	1525 1530 1535	
45	cta cga aga ctg gag aaa aag aga agg aaa gcc cag tgc aaa cct tac	4656
	Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys Pro Tyr	
	1540 1545 1550	
50	tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg tgc acc	4704
	Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu Cys Thr	
	1555 1560 1565	
55	agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg aac gtg	4752
	Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val	
	1570 1575 1580	
60	gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg gat gag	4800
	Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu	
	1585 1590 1595 1600	
65	gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc ttg gag	4848
	Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val Leu Glu	
	1605 1610 1615	
70	tca gtt ttc aaa ctt gtg gcc ttc ggt ttc cgt cgg ttc ttc cag gac	4896
	Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp	
	1620 1625 1630	
75	agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc atg ggc	4944
	Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly	
	1635 1640 1645	

	atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc aac ccc	4992
	Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile Asn Pro	
	1650 1655 1660	
5	acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg ctg aag	5040
	Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys	
	1665 1670 1675 1680	
10	ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg gtg atg	5088
	Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr Val Met	
	1685 1690 1695	
15	cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg ttg ttg	5136
	Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu	
	1700 1705 1710	
20	ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac ctg gag	5184
	Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu	
	1715 1720 1725	
25	tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc acc ttt	5232
	Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe	
	1730 1735 1740	
30	cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc aca ggt	5280
	Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly	
	1745 1750 1755 1760	
35	gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt gac cag	5328
	Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln	
	1765 1770 1775	
40	gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt gtg tcc	5376
	Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser	
	1780 1785 1790	
45	ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc gcc gtg	5424
	Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile Ala Val	
	1795 1800 1805	
50	ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag gag gcc	5472
	Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala	
	1810 1815 1820	
55	gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc ccc cag	5520
	Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln	
	1825 1830 1835 1840	
60	ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc gag ggc	5568
	Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly	
	1845 1850 1855	
65	ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca gcg gcc	5616
	Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro Ala Ala	
	1860 1865 1870	
70	cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg atg cag	5664
	His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr Met Gln	
	1875 1880 1885 1890	
75	ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg cgg aag	5712
	Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val Arg Lys	
	1890 1895 1900	

	tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac atg tgt	5760
	Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys	
	1905 1910 1915 1920	
5	cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc tgg ggg	5808
	Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly Trp Gly	
	1925 1930 1935	
10	ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc cag cca	5856
	Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser Gln Pro	
	1940 1945 1950	
15	gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct cat ctg	5904
	Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro His Leu	
	1955 1960 1965	
20	ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa ctg ccc	5952
	Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys Leu Pro	
	1970 1975 1980	
25	cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc cag gca	6000
	Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala	
	1985 1990 1995 2000	
30	gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc cgg gaa	6048
	Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu	
	2005 2010 2015	
35	gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc cgg gcc	6096
	Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala Arg Ala	
	2020 2025 2030	
40	tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac tcc cgc	6144
	Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His Ser Arg	
	2035 2040 2045	
45	agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct tgc cca	6192
	Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro Cys Pro	
	2050 2055 2060	
50	ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga agc agc	6240
	Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg Ser Ser	
	2065 2070 2075 2080	
55	tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc ctg ccc	6288
	Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro	
	2085 2090 2095	
60	cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag aag tgc	6336
	Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys Lys Cys	
	2100 2105 2110	
65	tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc tgg ctg	6384
	Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser Trp Leu	
	2115 2120 2125	
70	gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac agc ggc	6432
	Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly	
	2130 2135 2140	
75	tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc cag cct	6480
	Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly Gln Pro	
	2145 2150 2155 2160	

	ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg cct agt	6523
	Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser	
	2165 2170 2175	
5	atc acc ata gac ccc ccc gag agc caa ggt cct cgg acc ccg ccc agt	6576
	Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro Pro Ser	
	2180 2185 2190	
10	cct ggt atc tgc ctc cgg agg agg gct ccg tcc agc gac tcc aag gat	6624
	Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser Lys Asp	
	2195 2200 2205	
15	ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc tcc cca	6672
	Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro Ser Pro	
	2210 2215 2220	
20	aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca gca gac	6720
	Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Ala Asp	
	2225 2230 2235 2240	
20	ctg gac ccc	6729
	Leu Asp Pro	
25	<210> 5	
	<211> 6762	
	<212> DNA	
	<213> Rattus sp.	
30	<220>	
	<221> CDS	
	<222> (1)..(6762)	
35	<400> 5	
	atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc	48
	Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro	
	1 5 10 15	
40	cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag	96
	Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln	
	20 25 30	
45	ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg	144
	Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala	
	35 40 45	
50	gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg	192
	Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu	
	50 55 60	
50	agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac	240
	Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn	
	65 70 75 80	
55	ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg	288
	Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val	
	85 90 95	
60	act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag	336
	Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln	
	100 105 110	
	cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt	384
	Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe	

	115								120								125								
5	gct	gtg	gaa	atg	gtg	gtg	aag	atg	gtg	gcc	ttg	ggc	atc	ttt	ggg	aag	432								
	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys									
	130						135						140												
10	aaa	tgt	tac	ctg	gga	gac	act	tgg	aac	cgg	ctt	gac	ttt	ttc	att	gtc	480								
	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val									
	145			150						155			160												
15	att	gca	ggg	atg	ctg	gag	tat	tcg	ctg	gac	ctg	cag	aac	gtc	agc	ttc	528								
	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe									
				165						170			175												
20	tcc	gca	gtc	agg	aca	gtc	cgt	gtg	ctg	cga	ccg	ctc	agg	gcc	att	aac	576								
	Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn									
				180			185						190												
25	cgg	gtg	ccc	agc	atg	cgc	att	ctc	gtc	aca	tta	ctg	ctg	gac	acc	ttg	624								
	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu									
	195						200						205												
30	cct	atg	ctg	ggc	aac	gtc	ctg	ctg	ctc	tgt	ttc	ttc	gtc	ttt	ttc	atc	672								
	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile									
	210						215						220												
35	ttt	ggc	atc	gtg	ggc	gtc	cag	ctg	tgg	gca	gga	ctg	ctt	cgc	aac	cgg	720								
	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg									
	225			230						235			240												
40	tgc	ttc	ctc	ccc	gag	aac	ttc	agc	ctc	ccc	ctg	agc	gtg	gac	ctg	gag	768								
	Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu									
				245						250			255												
45	cct	tat	tac	cag	aca	gag	aat	gag	gac	gag	agc	ccc	ttc	atc	tgc	tct	816								
	Pro	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser									
				260			265						270												
50	cag	cct	cgg	gag	aat	ggc	atg	aga	tcc	tgc	agg	agt	gtg	ccc	aca	ctg	864								
	Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu									
	275						280						285												
55	cgt	ggg	gaa	ggc	ggt	ggt	ggc	cca	ccc	tgc	agt	ctg	gac	tat	gag	acc	912								
	Arg	Gly	Glu	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Ser	Leu	Asp	Tyr	Glu	Thr									
	290						295						300												
60	tat	aac	agt	tcc	agc	aac	acc	acc	tgt	gtc	aac	tgg	aac	cag	tac	tat	960								
	Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr									
	305			310						315			320												
65	acc	aac	tgc	tct	gcg	ggc	gag	cac	aac	ccc	ttc	aaa	ggc	gcc	atc	aac	1008								
	Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn									
				325						330			335												
70	ttt	gac	aac	att	ggc	tat	gcc	tgg	atc	gcc	atc	ttc	cag	gtc	atc	aca	1056								
	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr									
				340			345						350												
75	ctg	gag	ggc	tgg	gtc	gac	atc	atg	tac	ttc	gta	atg	gac	gct	cac	tcc	1104								
	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser									
	355						360						365												
80	ttc	tac	aac	ttc	atc	tac	ttc	att	ctt	ctc	atc	atc	gtg	ggc	tcc	ttc	1152								
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe									



	370	375	380	
5	ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu 385 390 395 400			1200
10	acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe 405 410 415			1248
15	ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys 420 425 430			1296
20	tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala 435 440 445			1344
25	cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu 450 455 460			1392
30	ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly 465 470 475 480			1440
35	agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His 485 490 495			1488
40	cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu 500 505 510			1536
45	aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly 515 520 525			1584
50	tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly 530 535 540			1632
55	ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp 545 550 555 560			1680
60	tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro 565 570 575			1728
65	tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr 580 585 590			1776
70	gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val 595 600 605			1824
75	gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile 610 615 620			1872
80	cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser 625 630 635			1920

	625				630					635					640	
5	acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag															1963
	Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys				645					650					655	
10	gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg															2016
	Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg				660					665					670	
15	aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca															2064
	Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser				675					680					685	
20	gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac															2112
	Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp				690										700	
25	ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat															2160
	Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp				705										720	
30	gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca															2208
	Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr				725										735	
35	ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc															2256
	Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile				740										750	
40	gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag															2304
	Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln				755										765	
45	ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc															2352
	Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr				770										780	
50	agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc															2400
	Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro				785										800	
55	ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg															2448
	Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val				805										815	
60	gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg															2496
	Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser				820										830	
65	gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc															2544
	Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe				835										845	
70	ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac															2592
	Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp				850										860	
75	aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc															2640
	Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe				865										880	
80	agc atc ctg ggc atg cat ctc ttc ggt tgc aag ttc gca tct gaa cgg															2688
	Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg				870											

	825	890	895	
5	gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp 900 905 910			2736
10	gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys 915 920 925			2784
15	gtc ctc tac aac ggc atg gcc tcc aca tcc tct tgg gct gct ctt tac Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr 930 935 940			2832
20	ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu 945 950 955 960			2880
25	gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys 965 970 975			2928
30	tct gag tca gag cct gat ttc ttt tcc agt gtg gat ggt gat ggg Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly 980 985 990			2976
35	gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu 995 1000 1005			3024
40	cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr 1010 1015 1020			3072
45	cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu 1025 1030 1035 1040			3120
50	ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly 1045 1050 1055			3168
55	gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro 1060 1065 1070			3216
60	cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser 1075 1080 1085			3264
65	agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser 1090 1095 1100			3312
70	ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat Gly Glu Arg Arg Ser Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp 1105 1110 1115 1120			3360
75	gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp 1125 1130 1135			3408
80	cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp 1140 1145 1150			3456

	1140	1145	1150	
5	ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly	1155	1160	1165 3504
10	cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tgg gct tca Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser	1170	1175	1180 3552
15	ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly	1185	1190	1195 1200 3600
20	gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln	1205	1210	1215 3648
25	gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser	1220	1225	1230 3696
30	tgg tgc gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys	1235	1240	1245 3744
35	cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile	1250	1255	1260 3792
40	atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp	1265	1270	1275 1280 3840
45	ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe	1285	1290	1295 3888
50	acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly	1300	1305	1310 3936
55	tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu	1315	1320	1325 3984
60	gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met	1330	1335	1340 4032
65	gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg	1345	1350	1355 1360 4080
70	ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly	1365	1370	1375 4128
75	ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly	1380	1385	1390 4176
80	aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu			4224

	1395	1400	1405	
5	ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp 1410 1415 1420	4272		
10	acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg 1425 1430 1435 1440	4320		
15	tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met 1445 1450 1455	4368		
20	tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr 1460 1465 1470	4416		
25	gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His 1475 1480 1485	4464		
30	aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala 1490 1495 1500	4512		
35	ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His 1505 1510 1515 1520	4560		
40	aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu 1525 1530 1535	4608		
45	aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln 1540 1545 1550	4656		
50	atg gcc gaa gcc cag tgc aag ccc tac tac tct gac tac tcg aga ttc Met Ala Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe 1555 1560 1565	4704		
55	cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac ctc ttc Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe 1570 1575 1580	4752		
60	atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg gaa cat Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His 1585 1590 1595 1600	4800		
65	tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc aat tac Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr 1605 1610 1615	4848		
70	atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala 1620 1625 1630	4896		
75	ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg gac ctg Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu 1635 1640 1645	4944		
80	gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag att gag Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu 1655 1660 1665	4992		

	1650	1655	1660	
5	gtc aat ctg tcg ctg ccc atc aac ccc acc atc atc cgt atc atg agg Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg 1665 1670 1675 1680	5040		
10	gtg ctc cgc att gct cga gtc ctg aag ctg ttg aag atg gct gtg ggc Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly 1685 1690 1695	5088		
15	atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag gtg ggg Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln Val Gly 1700 1705 1710	5136		
20	aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca gct ctg Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu 1715 1720 1725	5184		
25	ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac cct tgt Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys 1730 1735 1740	5232		
30	gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg gcc ttt Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe 1745 1750 1755 1760	5280		
35	ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt att atg Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met 1765 1770 1775	5328		
40	aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac act Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr 1780 1785 1790	5376		
45	gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe 1795 1800 1805	5424		
50	gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg gaa gaa Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu 1810 1815 1820	5472		
55	agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag ctg gag Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu 1825 1830 1835 1840	5520		
60	ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg ggc agc Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser 1845 1850 1855	5568		
65	ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac agc cct Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro 1860 1865 1870	5616		
70	aag cct ggg gct cca cac acc act gcc cac att gga gca gcc tcg ggc Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala Ser Gly 1875 1880 1885	5664		
75	ttc tcc ctt gag cac ccc acg atg gta ccc cac ccc gag gag gtg cca Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu Val Pro 1890 1895 1900	5712		
80	gtc ccc cta gga cca gac ctg ctg act gtg agg aag tct ggt gtc agc Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser 1905 1910 1915	5760		

	1905	1910	1915	1920	
5	cgg acg cac tct ctg ccc Arg Thr His Ser Leu Pro	aat gac agc tac atg tgc cgc Asn Asp Ser Tyr Met Cys Arg	aat ggg ago Asn Gly Ser	5803	
10	act gct gag aga tcc cta gga cac agg ggc tgg ggg ctc ccc aaa gcc Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala	1925 1940	1930 1945	1935 1950	5856
15	cag tca ggc tcc atc ttg tcc gtt cac tcc caa cca gca gac acc ago Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser	1955 1960	1965	5904	
20	tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg ctc cag cct cat Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln Pro His	1970 1975	1980	5952	
25	ggg gct ccc acc tgg ggc gcc atc cct aaa cta ccc cca cct ggc cgc Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg	1985 1990	1995	2000	6000
30	tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata agg act Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr	2005	2010	2015	6048
35	gac tcc ctg gat gtg cag ggc ctg ggt agc cgg gaa gac ctg ttg tca Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser	2020	2025	2030	6096
40	gag gtg agt ggg ccc tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp	2035	2040	2045	6144
45	ggc ggg tgc agc atc cag gtg cag cag cgt tcc ggc atc cag agc aaa Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys	2050 2055	2060	6192	
50	gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro	2065 2070	2075	2080	6240
55	agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag ctg gac Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp	2085	2090	2095	6288
60	acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc cag gaa Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu	2100	2105	2110	6336
65	gaa ccc ctg ttc cca cgg gac ctg aag aag tgc tac agt gta gag acc Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr	2115 2120	2125	6384	
70	cag agc tgc agg cgc agg cct ggg ttc tgg cta gat gaa cag cgg aga Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg	2130 2135	2140	6432	
75	cac tcc att gct gtc agc tgt ctg gac agc ggc tcc caa ccc cgc cta His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu	2145 2150	2155	2160	6480
80	tgt cca agc ccc tca agc ctc ggg ggc caa cct ctt ggg ggt cct ggg Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly	6528			

2165 2170 2175

5 agc cgg cct aag aaa aaa ctc agc cca ccc agt atc tct ata gac ccc 6576  
 Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro  
 2180 2185 2190

10 ccg gag agc cag ggc tct cgg ccc cca tgc agt cct ggt gtc tgc ctc 6624  
 Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu  
 2195 2200 2205

agg agg agg gcg ccg gcc agt gac tct aag gat ccc tcg gtc tcc agc 6672  
 Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser  
 2210 2215 2220

15 ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac acg ctg 6720  
 Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu  
 2225 2230 2235 2240

20 agt ctc tct ggt ttg tct tct gac cca aca gac atg gac ccc 6762  
 Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro  
 2245 2250

25 <210> 6  
 <211> 6795  
 <212> DNA  
 <213> Rattus sp.

30 <220>  
 <221> CDS  
 <222> (1)..(6795)

35 <400> 6  
 atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc 48  
 Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro  
 1 5 10 15

40 cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg gcc cgg cag 96  
 Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln  
 20 25 30

45 ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144  
 Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala  
 35 40 45

50 gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192  
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu  
 50 55 60

55 agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240  
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn  
 65 70 75 80

60 ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg 288  
 Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val  
 85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336  
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln  
 100 105 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt 384  
 Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe  
 115 120 125



	gct	gtg	gaa	atg	gtg	gtg	aag	atg	gtg	gcc	ttg	ggc	atc	ttt	ggg	aag	432
	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	
	130						135					140					
5	aaa	tgt	tac	ctg	gga	gac	act	tgg	aac	cgg	ctt	gac	ttt	ttc	att	gtc	480
	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val	
	145					150					155					160	
10	att	gca	ggg	atg	ctg	gag	tat	tgg	ctg	gac	ctg	cag	aac	gtc	agc	ttc	528
	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe	
					165					170					175		
15	tcc	gca	gtc	agg	aca	gtc	cgt	gtg	ctg	cga	ccg	ctc	agg	gcc	att	aac	576
	Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn	
				180					185					190			
20	cgg	gtg	ccc	agc	atg	cgc	att	ctc	gtc	aca	tta	ctg	ctg	gac	acc	ttg	624
	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu	
			195					200					205				
25	cct	atg	ctg	ggc	aac	gtc	ctg	ctg	ctc	tgt	ttc	ttc	gtc	ttt	ttc	atc	672
	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	
	210					215						220					
30	ttt	ggc	atc	gtg	ggc	gtc	cag	ctg	tgg	gca	gga	ctg	ctt	cgc	aac	cgg	720
	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	
	225					230					235					240	
35	tgc	ttc	ctc	ccc	gag	aac	ttc	agc	ctc	ccc	ctg	agc	gtg	gac	ctg	gag	768
	Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu	
					245					250					255		
40	cct	tat	tac	cag	aca	gag	aat	gag	gac	gag	agc	ccc	ttc	atc	tgc	tct	816
	Pro	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser	
				260					265					270			
45	cag	cct	cgg	gag	aat	ggc	atg	aga	tcc	tgc	agg	agt	gtg	ccc	aca	ctg	864
	Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu	
			275					280					285				
50	cgt	ggg	gaa	ggc	ggt	ggt	ggc	cca	ccc	tgc	agt	ctg	gac	tat	gag	acc	912
	Arg	Gly	Glu	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Ser	Leu	Asp	Tyr	Glu	Thr	
	290					295						300					
55	tat	aac	agt	tcc	agc	aac	acc	acc	tgt	gtc	aac	tgg	aac	cag	tac	tat	960
	Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr	
	305					310					315					320	
60	acc	aac	tgc	tct	gcg	ggc	gag	cac	aac	ccc	ttc	aaa	ggc	gcc	atc	aac	1008
	Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn	
					325					330					335		
65	ttt	gac	aac	att	ggc	tat	gcc	tgg	atc	gcc	atc	ttc	cag	gtc	atc	aca	1056
	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr	
				340				345						350			
70	ctg	gag	ggc	tgg	gtc	gac	atc	atg	tac	ttc	gta	atg	gac	gct	cac	tcc	1104
	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser	
			355					360					365				
75	ttc	tac	aac	ttc	atc	tac	ttc	att	ctt	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
			370				375					380					

5	ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag	1200
	Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu	
	385 390 395 400	
10	acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc	1248
	Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe	
	405 410 415	
15	ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc	1296
	Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys	
	420 425 430	
20	tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc	1344
	Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala	
	435 440 445	
25	cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg	1392
	Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu	
	450 455 460	
30	ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc	1440
	Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly	
	465 470 475 480	
35	agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac	1488
	Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His	
	485 490 495	
40	cac cat cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc	1536
	His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu	
	500 505 510	
45	aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg	1584
	Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly	
	515 520 525	
50	tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg	1632
	Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly	
	530 535 540	
55	ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac	1680
	Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp	
	545 550 555 560	
60	tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca	1728
	Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro	
	565 570 575	
65	tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act	1776
	Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr	
	580 585 590	
70	gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg	1824
	Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val	
	595 600 605	
75	gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc	1872
	Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile	
	610 615 620	
80	cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt	1920
	Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser	
	625 630 635 640	

	acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag	1968
	Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys	
	645 650 655	
5		
	gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg	2016
	Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg	
	660 665 670	
10		
	aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca	2064
	Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser	
	675 680 685	
15		
	gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac	2112
	Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp	
	690 695 700	
20		
	ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat	2160
	Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp	
	705 710 715 720	
25		
	gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca	2208
	Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr	
	725 730 735	
30		
	ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc	2256
	Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile	
	740 745 750	
35		
	gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag	2304
	Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln	
	755 760 765	
40		
	ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc	2352
	Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr	
	770 775 780	
45		
	agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc	2400
	Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro	
	785 790 795 800	
50		
	ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg	2448
	Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val	
	805 810 815	
55		
	gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg	2496
	Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser	
	820 825 830	
60		
	gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc	2544
	Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe	
	835 840 845	
65		
	ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac	2592
	Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp	
	850 855 860	
70		
	aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc	2640
	Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe	
	865 870 875 880	
75		
	agc atc ctg ggc atg cat ctc ttc ggt tgc aag ttc gca tct gaa cgg	2688
	Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg	
	885 890 895	

	gat	ggg	gac	acg	ttg	cca	gac	cgg	aag	aat	ttc	gac	tcc	ctg	ctc	tgg	2736
	Asp	Gly	Asp	Thr	Leu	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp	
				900					905					910			
5	gcc	atc	gtc	act	gtc	ttt	cag	att	ctg	act	cag	gaa	gac	tgg	aat	aaa	2784
	Ala	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Lys	
			915					920					925				
10	gtc	ctc	tac	aac	ggc	atg	gcc	tcc	aca	tgc	tct	tgg	gct	gct	ctt	tac	2832
	Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr	
			930				935					940					
15	ttc	atc	gcc	ctc	atg	act	ttt	ggc	aac	tat	gtg	ctc	ttt	aac	ctg	ctg	2880
	Phe	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	
	945					950					955					960	
20	gtg	gcc	att	ctt	gtg	gaa	gga	ttc	cag	gca	gag	gga	gat	gcc	acc	aag	2928
	Val	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Gly	Asp	Ala	Thr	Lys	
					965					970					975		
25	tct	gag	tca	gag	cct	gat	ttc	ttt	tgc	ccc	agt	gtg	gat	ggc	gat	ggg	2976
	Ser	Glu	Ser	Glu	Pro	Asp	Phe	Phe	Ser	Pro	Ser	Val	Asp	Gly	Asp	Gly	
				980					985					990			
30	gac	aga	aag	aag	cgc	ttg	gcc	ctg	gtg	gct	ttg	gga	gaa	cac	gcg	gaa	3024
	Asp	Arg	Lys	Lys	Arg	Leu	Ala	Leu	Val	Ala	Leu	Gly	Glu	His	Ala	Glu	
			995					1000					1005				
35	cta	cga	aag	agc	ctt	ttg	cca	ccc	ctc	atc	atc	cat	acg	gct	gcg	aca	3072
	Leu	Arg	Lys	Ser	Leu	Leu	Pro	Pro	Leu	Ile	Ile	His	Thr	Ala	Ala	Thr	
		1010					1015					1020					
40	cca	atg	tca	cac	ccc	aag	agc	tcc	agc	aca	ggt	gtg	ggg	gaa	gca	ctg	3120
	Pro	Met	Ser	His	Pro	Lys	Ser	Ser	Ser	Thr	Gly	Val	Gly	Glu	Ala	Leu	
		1025				1030					1035					1040	
45	ggc	tct	ggc	tct	cga	cgt	acc	agt	agc	agt	ggg	tcc	gct	gag	cct	gga	3168
	Gly	Ser	Gly	Ser	Arg	Arg	Thr	Ser	Ser	Ser	Gly	Ser	Ala	Glu	Pro	Gly	
					1045					1050					1055		
50	gct	gcc	cac	cat	gag	atg	aaa	tgt	ccg	cca	agt	gcc	cgc	agc	tcc	ccg	3216
	Ala	Ala	His	His	Glu	Met	Lys	Cys	Pro	Pro	Ser	Ala	Arg	Ser	Ser	Pro	
				1060				1065					1070				
55	cac	agt	ccc	tgg	agt	gcg	gca	agc	agc	tgg	acc	agc	agg	cgc	tcc	agc	3264
	His	Ser	Pro	Trp	Ser	Ala	Ala	Ser	Ser	Trp	Thr	Ser	Arg	Arg	Ser	Ser	
			1075				1080					1085					
60	agg	aac	agc	ctg	ggc	cgg	gcc	ccc	agc	cta	aag	cgg	agg	agc	ccg	agc	3312
	Arg	Asn	Ser	Leu	Gly	Arg	Ala	Pro	Ser	Leu	Lys	Arg	Arg	Ser	Pro	Ser	
		1090					1095					1100					
65	ggg	gag	cgg	agg	tcc	ctg	ctg	tct	gga	gag	ggc	cag	gag	agt	cag	gat	3360
	Gly	Glu	Arg	Arg	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gln	Glu	Ser	Gln	Asp	
		1105				1110					1115					1120	
70	gag	gag	gaa	agt	tca	gaa	gag	gac	cgg	gcc	agc	cca	gca	ggc	agt	gac	3408
	Glu	Glu	Glu	Ser	Ser	Glu	Glu	Asp	Arg	Ala	Ser	Pro	Ala	Gly	Ser	Asp	
					1125					1130					1135		
75	cat	cgc	cac	agg	ggc	tcc	ttg	gaa	cgt	gag	gcc	aag	agt	tcc	ttt	gac	3456
	His	Arg	His	Arg	Gly	Ser	Leu	Glu	Arg	Glu	Ala	Lys	Ser	Ser	Phe	Asp	
					1140				1145					1150			

	ctg cct gac act ctg cag gtg cgg ggg ctg cac cgc aca gcc agc ggc	3504
	Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly	
	1155 1160 1165	
5	egg agc tct gcc tct gag cac caa gac tgt aat ggc aag tgg gct tca	3552
	Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser	
	1170 1175 1180	
10	ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg	3600
	Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly	
	1185 1190 1195 1200	
15	gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa	3648
	Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln	
	1205 1210 1215	
20	gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc	3696
	Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser	
	1220 1225 1230	
25	tgg tgg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt	3744
	Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys	
	1235 1240 1245	
30	cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc	3792
	His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile	
	1250 1255 1260	
35	atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac	3840
	Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp	
	1265 1270 1275 1280	
40	ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc	3888
	Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe	
	1285 1290 1295	
45	acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc	3936
	Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly	
	1300 1305 1310	
50	tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg	3984
	Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu	
	1315 1320 1325	
55	gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg	4032
	Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met	
	1330 1335 1340	
60	gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg	4080
	Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg	
	1345 1350 1355 1360	
65	ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga	4128
	Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly	
	1365 1370 1375	
70	ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc	4176
	Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly	
	1380 1385 1390	
75	aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc	4224
	Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu	
	1395 1400 1405	

	ggg gtc cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac	4272
	Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp	
	1410 1415 1420	
5	acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga	4320
	Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg	
	1425 1430 1435 1440	
10	tgg gtc cgg cac aag tac aac ttt gac aac ctg gcc cag gct ctg atg	4368
	Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met	
	1445 1450 1455	
15	tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat	4416
	Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr	
	1460 1465 1470	
20	gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac	4464
	Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His	
	1475 1480 1485	
25	aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc	4512
	Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala	
	1490 1495 1500	
	ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat	4560
	Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His	
	1505 1510 1515 1520	
30	aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag	4608
	Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu	
	1525 1530 1535	
35	aag cga cta cgg agg ctg gag aaa aag aga agg aat cta atg ttg gac	4656
	Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp	
	1540 1545 1550	
40	gat gta att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag	4704
	Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln	
	1555 1560 1565	
45	tgc aag ccc tac tac tct gac tac tcg aga ttc cgg ctc ctt gtc cac	4752
	Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His	
	1570 1575 1580	
	cac ctg tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc	4800
	His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile	
	1585 1590 1595 1600	
50	ggg ctg aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag	4848
	Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln	
	1605 1610 1615	
55	atc ctg gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc	4896
	Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile	
	1620 1625 1630	
60	ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt	4944
	Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg	
	1635 1640 1645	
	ttc ttc cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg	4992
	Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu	
	1650 1655 1660	

5	<p> tcc atc atg ggc atc aca ctg gag gag att gag gtc aat ctg tct ctg 5040  Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu  1665 1670 1675 1680 </p> <p> ccc atc aac ccc acc atc atc cgt atc atg agg gtg ctc cgc att gct 5088  Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala  1685 1690 1695 </p>
10	<p> cga gtt ctg aag ctg ttg aag atg gct gtg ggc atg cgg gca ctg ctg 5136  Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu  1700 1705 1710 </p>
15	<p> cac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc 5184  His Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu  1715 1720 1725 </p>
20	<p> ttc atg tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttc 5232  Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe  1730 1735 1740 </p>
25	<p> gga gac ctg gag tgt gat gag aca cac cct tgt gag ggc ttg ggt cgg 5280  Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg  1745 1750 1755 1760 </p>
30	<p> cat gcc acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga 5328  His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg  1765 1770 1775 </p>
35	<p> gtc tcc act ggt gac aac tgg aat ggt att atg aag gac acc ctc cgg 5376  Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg  1780 1785 1790 </p>
40	<p> gac tgt gac cag gag tcc acc tgc tac aac act gtc atc tcc cct atc 5424  Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile  1795 1800 1805 </p>
45	<p> tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg 5472  Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val  1810 1815 1820 </p>
50	<p> gtc ata gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc 5520  Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala  1825 1830 1835 1840 </p>
55	<p> aag gag gag gcc gag ctc gag gcc gag ctg gag ctg gag atg aag acg 5568  Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr  1845 1850 1855 </p>
60	<p> ctc agc ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc 5616  Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro  1860 1865 1870 </p>
65	<p> ggg gtg gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca 5664  Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro  1875 1880 1885 </p>
70	<p> cac acc act gcc cac att gga gca gcc tct ggc ttc tcc ctt gag cac 5712  His Thr Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His  1890 1895 1900 </p>
75	<p> ccc acg atg gta ccc cac ccc gag gag gtg cca gtc ccc cta gga cca 5760  Pro Thr Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro  1905 1910 1915 1920 </p>

	gac ctg ctg act gtg agg aag tct ggt gtc agc cgg acg cac tct ctg	5808
	Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu	
	1925 1930 1935	
5	ccc aat gac agc tac atg tgc cgc aat ggg agc act gct gag aga tcc	5856
	Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser	
	1940 1945 1950	
10	cta gga cac agg ggc tgg ggg ctc ccc aaa gcc cag tca ggc tcc atc	5904
	Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile	
	1955 1960 1965	
15	ttg tcc gtt cac tcc caa cca gca gac acc agc tgc atc cta cag ctt	5952
	Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu	
	1970 1975 1980	
20	ccc aaa gat gtg cac tat ctg ctc cag cct cat ggg gct ccc acc tgg	6000
	Pro Lys Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp	
	1985 1990 1995 2000	
25	ggc gcc atc cct aaa cta ccc cca cct ggc cgc tcc cct ctg gct cag	6048
	Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln	
	2005 2010 2015	
30	agg cct ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg	6096
	Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val	
	2020 2025 2030	
35	cag ggc ctg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc	6144
	Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro	
	2035 2040 2045	
40	tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg tgc agc atc	6192
	Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile	
	2050 2055 2060	
45	cag gtg cag cag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc	6240
	Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile	
	2065 2070 2075 2080	
50	cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc agc tgg gcc aag gac	6288
	Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp	
	2085 2090 2095	
55	cct cca gag acc aga agc agc tta gag ctg gac acg gag ctg agc tgg	6336
	Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp	
	2100 2105 2110	
60	att tca gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttc cca	6384
	Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro	
	2115 2120 2125	
65	cgg gac ctg aag aag tgc tac agt gta gag acc cag agc tgc agg cgc	6432
	Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg	
	2130 2135 2140	
70	agg cct ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gct gtc	6480
	Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val	
	2145 2150 2155 2160	
75	agc tgt ctg gac agc ggc tcc caa ccc cgc cta tgt cca agc ccc tca	6528
	Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser	
	2165 2170 2175	



agc ctc ggg ggc aac cct ctt ggg ggt cct ggg agc cgg cct aag aaa 6576  
 Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys  
 2180 2185 2190

5 aaa ctc agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc 6624  
 Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly  
 2195 2200 2205

10 tct cgg ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg 6672  
 Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro  
 2210 2215 2220

15 gcc agt gac tct aag gat ccc tcg gtc tcc agc ccc ctt gac agc acg 6720  
 Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr  
 2225 2230 2235 2240

20 gct gcc tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg 6768  
 Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu  
 2245 2250 2255

25 tct tct gac cca aca gac atg gac ccc 6795  
 Ser Ser Asp Pro Thr Asp Met Asp Pro  
 2260 2265

30 <210> 7  
 <211> 6816  
 <212> DNA  
 <213> Rattus sp.  
 <220>  
 <221> CDS  
 <222> (1)...(6816)

35 <400> 7  
 atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc 48  
 Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro  
 1 5 10 15

40 cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc ccg cag 96  
 Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln  
 20 25 30

45 ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144  
 Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala  
 35 40 45

50 gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192  
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu  
 50 55 60

55 agc cag gac agc cgc ccg ccg agc tgg tgt ctc cgc acg gtc tgt aac 240  
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn  
 65 70 75 80

60 ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg 288  
 Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val  
 85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336  
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln  
 100 105 110

	cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttc gcc ttc ttc	384
	Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe	
	115 120 125	
5	gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag	432
	Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys	
	130 135 140	
10	aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc	480
	Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val	
	145 150 155 160	
15	att gca ggg atg ctg gag tat tgc ctg gac ctg cag aac gtc agc ttc	528
	Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe	
	165 170 175	
20	tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac	576
	Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn	
	180 185 190	
25	cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg	624
	Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu	
	195 200 205	
30	cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc	672
	Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile	
	210 215 220	
35	ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg	720
	Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg	
	225 230 235 240	
40	tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag	768
	Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu	
	245 250 255	
45	cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct	816
	Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser	
	260 265 270	
50	cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg	864
	Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu	
	275 280 285	
55	cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc	912
	Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr	
	290 295 300	
60	tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat	960
	Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr	
	305 310 315 320	
65	acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac	1008
	Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn	
	325 330 335	
70	ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca	1056
	Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr	
	340 345 350	
75	ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc	1104
	Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser	
	355 360 365	

	ttc	tac	aac	ttc	atc	tac	ttc	att	ctt	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
	370						375					380					
5	ttc	atg	atc	aac	ctg	tgc	ctg	gtg	gtg	att	gcc	acg	cag	ttc	tcc	gag	1200
	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu	
	385					390					395					400	
10	acc	aaa	cag	cgg	gag	agt	cag	ctg	atg	cgg	gag	cag	cgt	gta	cga	ttc	1248
	Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe	
					405					410					415		
15	ctg	tcc	aat	gct	agc	acc	ctg	gca	agc	ttc	tct	gag	cca	ggc	agc	tgc	1296
	Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys	
				420					425					430			
20	tat	gag	gag	cta	ctc	aag	tac	ctg	gtg	tac	atc	ctc	cga	aaa	gca	gcc	1344
	Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala	
			435					440					445				
	cga	agg	ctg	gcc	cag	gtc	tct	agg	gct	ata	ggc	gtg	cgg	gct	ggg	ctg	1392
	Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ile	Gly	Val	Arg	Ala	Gly	Leu	
	450						455					460					
25	ctc	agc	agc	cca	gtg	gcc	cgt	agt	ggg	cag	gag	ccc	cag	ccc	agt	ggc	1440
	Leu	Ser	Ser	Pro	Val	Ala	Arg	Ser	Gly	Gln	Glu	Pro	Gln	Pro	Ser	Gly	
	465					470					475					480	
30	agc	tgc	act	cgc	tca	cac	cgt	cgt	ctg	tct	gtc	cac	cac	ctg	gtc	cac	1488
	Ser	Cys	Thr	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His	
					485					490					495		
35	cac	cat	cac	cac	cac	cat	cac	cac	tac	cac	ctg	ggg	aat	ggg	acg	ctc	1536
	His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu	
				500					505					510			
40	aga	gtt	ccc	cgg	gcc	agc	cca	gag	atc	cag	gac	agg	gat	gcc	aat	ggg	1584
	Arg	Val	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly	
			515					520					525				
	tct	cgc	cgg	ctc	atg	cta	cca	cca	ccc	tct	aca	ccc	act	ccc	tct	ggg	1632
	Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr	Pro	Thr	Pro	Ser	Gly	
	530						535					540					
45	ggc	cct	ccg	agg	ggg	gcg	gag	tct	gta	cac	agc	ttc	tac	cat	gct	gac	1680
	Gly	Pro	Pro	Arg	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp	
	545				550						555					560	
50	tgc	cac	ttg	gag	cca	gtc	cgt	tgc	cag	gca	ccc	cct	ccc	aga	tgc	cca	1728
	Cys	His	Leu	Glu	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Cys	Pro	
					565					570					575		
55	tgc	gag	gca	tct	ggg	agg	act	gtg	ggg	agt	ggg	aag	gtg	tac	ccc	act	1776
	Ser	Glu	Ala	Ser	Gly	Arg	Thr	Val	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr	
				580					585					590			
60	gtg	cat	acc	agc	cct	cca	cca	gag	ata	ctg	aag	gat	aaa	gca	cta	gtg	1824
	Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Ile	Leu	Lys	Asp	Lys	Ala	Leu	Val	
			595					600					605				
	gag	gtg	gcc	ccc	agc	cct	ggg	ccc	ccc	acc	ctc	acc	agc	ttc	aac	atc	1872
	Glu	Val	Ala	Pro	Ser	Pro	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Phe	Asn	Ile	
	610						615					620					

	cca	cct	ggg	ccc	ttc	agc	tcc	atg	cac	aag	ctc	ctg	gag	aca	cag	agt	1920
	Pro	Pro	Gly	Pro	Phe	Ser	Ser	Met	His	Lys	Leu	Leu	Glu	Thr	Gln	Ser	
	625					630					635					640	
5	acg	gga	gcc	tgc	cat	agc	tcc	tgc	aaa	atc	tcc	agc	cct	tgc	tcc	aag	1968
	Thr	Gly	Ala	Cys	His	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Ser	Lys	
					645					650						655	
10	gca	gac	agt	gga	gcc	tgc	ggg	ccg	gac	agt	tgt	ccc	tac	tgt	gcc	cgg	2016
	Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pro	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg	
				660					665					670			
15	aca	gga	gca	gga	gag	cca	gag	tcc	gct	gac	cat	gtc	atg	cct	gac	tca	2064
	Thr	Gly	Ala	Gly	Glu	Pro	Glu	Ser	Ala	Asp	His	Val	Met	Pro	Asp	Ser	
				675				680					685				
20	gac	agc	gag	gct	gtg	tat	gag	ttc	aca	cag	gac	gct	cag	cac	agt	gac	2112
	Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp	
		690					695					700					
25	ctc	cgg	gat	ccc	cac	agc	cgg	cgg	cga	cag	cgg	agc	ctg	ggc	cca	gat	2160
	Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	
	705					710					715					720	
30	gca	gag	cct	agt	tct	gtg	ctg	gct	ttc	tgg	agg	ctg	atc	tgt	gac	aca	2208
	Ala	Glu	Pro	Ser	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	
					725					730					735		
35	ttc	cgg	aag	atc	gta	gat	agc	aaa	tac	ttt	ggc	cgg	gga	atc	atg	atc	2256
	Phe	Arg	Lys	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	
				740					745					750			
40	gcc	atc	ctg	gtc	aat	aca	ctc	agc	atg	ggc	atc	gag	tac	cac	gag	cag	2304
	Ala	Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	Glu	Tyr	His	Glu	Gln	
			755					760					765				
45	ccc	gag	gag	ctc	acc	aac	gcc	ctg	gaa	atc	agc	aac	atc	gtc	ttc	acc	2352
	Pro	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr	
		770					775					780					
50	agc	ctc	ttc	gcc	ttg	gag	atg	ctg	ctg	aaa	ctg	ctt	gtc	tac	ggc	ccc	2400
	Ser	Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	
	785				790						795					800	
55	ttt	ggc	tac	att	aag	aat	ccc	tac	aac	atc	ttt	gat	ggc	gtc	att	gtg	2448
	Phe	Gly	Tyr	Ile	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	
				805						810					815		
60	gtc	atc	agt	gtg	tgg	gag	att	gtg	ggc	cag	cag	gga	ggc	ggc	ctg	tcg	2496
	Val	Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser	
				820					825					830			
65	gtg	ctg	cgg	acc	ttc	cgc	ctg	atg	cgg	gtg	ctg	aag	ctg	gtg	cgc	ttc	2544
	Val	Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	
			835					840					845				
70	ctg	ccg	gcc	ctg	cag	cgc	cag	ctc	gtg	gtg	ctc	atg	aag	acc	atg	gac	2592
	Leu	Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	
		850					855					860					
75	aac	gtg	gcc	acc	ttc	tgc	atg	ctc	ctc	atg	ctg	ttc	atc	ttc	atc	ttc	2640
	Asn	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	
	865					870					875					880	

	agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg	2688
	Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg	
	385 890 895	
5	gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg	2736
	Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp	
	900 905 910	
10	gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa	2784
	Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys	
	915 920 925	
15	gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac	2832
	Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr	
	930 935 940	
20	ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg	2880
	Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu	
	945 950 955 960	
25	gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag	2928
	Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys	
	965 970 975	
30	tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg	2976
	Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly	
	980 985 990	
35	gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa	3024
	Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu	
	995 1000 1005	
40	cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca	3072
	Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr	
	1010 1015 1020	
45	cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg	3120
	Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu	
	1025 1030 1035 1040	
50	ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga	3168
	Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly	
	1045 1050 1055	
55	gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg	3216
	Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Pro	
	1060 1065 1070	
60	cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc	3264
	His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser	
	1075 1080 1085	
65	agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc	3312
	Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser	
	1090 1095 1100	
70	ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat	3360
	Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp	
	1105 1110 1115 1120	
75	gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac	3408
	Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp	
	1125 1130 1135	

	cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac	3456
	His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp	
	1140 1145 1150	
5	ctg cct gac act ctg cag gtg cgg ggg ctg cac cgc aca gcc agc ggc	3504
	Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly	
	1155 1160 1165	
10	cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tgg gct tca	3552
	Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser	
	1170 1175 1180	
15	ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg	3600
	Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly	
	1185 1190 1195 1200	
20	gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa	3648
	Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln	
	1205 1210 1215	
	gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc	3696
	Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser	
	1220 1225 1230	
25	tgg tgg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt	3744
	Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys	
	1235 1240 1245	
30	cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc	3792
	His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile	
	1250 1255 1260	
35	atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac	3840
	Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp	
	1265 1270 1275 1280	
40	ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc	3888
	Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe	
	1285 1290 1295	
	acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc	3936
	Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly	
	1300 1305 1310	
45	tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg	3984
	Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu	
	1315 1320 1325	
50	gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg	4032
	Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met	
	1330 1335 1340	
55	gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg	4080
	Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg	
	1345 1350 1355 1360	
	ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga	4128
	Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly	
	1365 1370 1375	
60	ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc	4176
	Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly	
	1380 1385 1390	

	aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc	4224
	Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu	
	1395 1400 1405	
5	ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac	4272
	Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp	
	1410 1415 1420	
10	acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga	4320
	Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg	
	1425 1430 1435 1440	
15	tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg	4368
	Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met	
	1445 1450 1455	
20	tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tac	4416
	Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr	
	1460 1465 1470	
25	gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac	4464
	Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His	
	1475 1480 1485	
30	aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc	4512
	Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala	
	1490 1495 1500	
35	ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat	4560
	Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His	
	1505 1510 1515 1520	
40	aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag	4608
	Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu	
	1525 1530 1535	
45	aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag	4656
	Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln	
	1540 1545 1550	
50	atg gcc gat cta atg ttg gac gat gra att gct tcc ggc agc tca gcc	4704
	Met Ala Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala	
	1555 1560 1565	
55	agc gct gcg tca gaa gcc cag tgc aag ccc tac tac tct gac tac tcg	4752
	Ser Ala Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser	
	1570 1575 1580	
60	aga ttc cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac	4800
	Arg Phe Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp	
	1585 1590 1595 1600	
65	ctc ttc atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg	4848
	Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met	
	1605 1610 1615	
70	gaa cat tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc	4896
	Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys	
	1620 1625 1630	
75	aat tac atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctc	4944
	Asn Tyr Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu	
	1635 1640 1645	

	gtg gcc ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg	4992
	Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu	
	1650 1655 1660	
5	gac ctg gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag	5040
	Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu	
	1665 1670 1675 1680	
10	att gag gtc aat ctg tgc ctg ccc atc aac ccc acc atc atc cgt atc	5088
	Ile Glu Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile	
	1685 1690 1695	
15	atg agg gtg ctc cgc att gct cga gtt ctg aag ctg ttg aag atg gct	5136
	Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala	
	1700 1705 1710	
20	gtg ggc atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag	5184
	Val Gly Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln	
	1715 1720 1725	
25	gtg ggg aac ctg gga ctc ctc ttc atg tta ttg ttt ttc atc ttt gca	5232
	Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala	
	1730 1735 1740	
30	gct ctg ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac	5280
	Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His	
	1745 1750 1755 1760	
35	cct tgt gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg	5328
	Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met	
	1765 1770 1775	
40	gcc ttt ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt	5376
	Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly	
	1780 1785 1790	
45	att atg aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac	5424
	Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr	
	1795 1800 1805	
50	aac act gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc	5472
	Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala	
	1810 1815 1820	
55	cag ttt gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg	5520
	Gln Phe Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu	
	1825 1830 1835 1840	
60	gaa gaa agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag	5568
	Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu	
	1845 1850 1855	
65	ctg gag ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg	5616
	Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu	
	1860 1865 1870	
70	ggc agc ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac	5664
	Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp	
	1875 1880 1885	
75	agc cct aag cct ggg gct cca cac acc act gcc cac att gga gca gcc	5712
	Ser Pro Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala	
	1890 1895 1900	



	tcc	ggc	ttc	tcc	ctt	gag	cac	ccc	acg	atg	gta	ccc	cac	ccc	gag	gag	5760
	Ser	Gly	Phe	Ser	Leu	Glu	His	Pro	Thr	Met	Val	Pro	His	Pro	Glu	Glu	
	1905					1910					1915					1920	
5	gtg	cca	gtc	ccc	cta	gga	cca	gac	ctg	ctg	act	gtg	agg	aag	tct	ggc	5808
	Val	Pro	Val	Pro	Leu	Gly	Pro	Asp	Leu	Leu	Thr	Val	Arg	Lys	Ser	Gly	
					1925					1930					1935		
10	gtc	agc	cgg	acg	cac	tct	ctg	ccc	aat	gac	agc	tac	atg	tgc	cgc	aat	5856
	Val	Ser	Arg	Thr	His	Ser	Leu	Pro	Asn	Asp	Ser	Tyr	Met	Cys	Arg	Asn	
				1940					1945					1950			
15	ggg	agc	act	gct	gag	aga	tcc	cta	gga	cac	agg	ggc	tgg	ggg	ctc	ccc	5904
	Gly	Ser	Thr	Ala	Glu	Arg	Ser	Leu	Gly	His	Arg	Gly	Trp	Gly	Leu	Pro	
		1955						1960					1965				
20	aaa	gcc	cag	tca	ggc	tcc	atc	ttg	tcc	gtt	cac	tcc	caa	cca	gca	gac	5952
	Lys	Ala	Gln	Ser	Gly	Ser	Ile	Leu	Ser	Val	His	Ser	Gln	Pro	Ala	Asp	
	1970						1975					1980					
	acc	agc	tgc	atc	cta	cag	ctt	ccc	aaa	gat	gtg	cac	tat	ctg	ctc	cag	6000
	Thr	Ser	Cys	Ile	Leu	Gln	Leu	Pro	Lys	Asp	Val	His	Tyr	Leu	Leu	Gln	
	1985				1990						1995					2000	
25	cct	cat	ggg	gct	ccc	acc	tgg	ggc	gcc	atc	cct	aaa	cta	ccc	cca	cct	6048
	Pro	His	Gly	Ala	Pro	Thr	Trp	Gly	Ala	Ile	Pro	Lys	Leu	Pro	Pro	Pro	
					2005					2010					2015		
30	ggc	cgc	tcc	cct	ctg	gct	cag	agg	cct	ctc	agg	cgc	cag	gca	gca	ata	6096
	Gly	Arg	Ser	Pro	Leu	Ala	Gln	Arg	Pro	Leu	Arg	Arg	Gln	Ala	Ala	Ile	
				2020					2025					2030			
35	agg	act	gac	tcc	ctg	gat	gtg	cag	ggc	ctg	ggc	agc	cgg	gaa	gac	ctg	6144
	Arg	Thr	Asp	Ser	Leu	Asp	Val	Gln	Gly	Leu	Gly	Ser	Arg	Glu	Asp	Leu	
		2035					2040					2045					
40	ttg	tca	gag	gtg	agt	ggg	ccc	tcc	tgc	cct	ctg	acc	cgg	tcc	tca	tcc	6192
	Leu	Ser	Glu	Val	Ser	Gly	Pro	Ser	Cys	Pro	Leu	Thr	Arg	Ser	Ser	Ser	
	2050					2055					2060						
	ttc	tgg	ggc	ggg	tgc	agc	atc	cag	gtg	cag	cag	cgt	tcc	ggc	atc	cag	6240
	Phe	Trp	Gly	Gly	Ser	Ser	Ile	Gln	Val	Gln	Gln	Arg	Ser	Gly	Ile	Gln	
	2065				2070					2075					2080		
45	agc	aaa	gtc	tcc	aag	cac	atc	cgc	ctg	cca	gcc	cct	tgc	cca	ggc	ctg	6288
	Ser	Lys	Val	Ser	Lys	His	Ile	Arg	Leu	Pro	Ala	Pro	Cys	Pro	Gly	Leu	
				2085					2090					2095			
50	gaa	ccc	agc	tgg	gcc	aag	gac	cct	cca	gag	acc	aga	agc	agc	tta	gag	6336
	Glu	Pro	Ser	Trp	Ala	Lys	Asp	Pro	Pro	Glu	Thr	Arg	Ser	Ser	Leu	Glu	
			2100					2105					2110				
55	ctg	gac	acg	gag	ctg	agc	tgg	att	tca	gga	gac	ctc	ctt	ccc	agc	agc	6384
	Leu	Asp	Thr	Glu	Leu	Ser	Trp	Ile	Ser	Gly	Asp	Leu	Leu	Pro	Ser	Ser	
		2115					2120					2125					
60	cag	gaa	gaa	ccc	ctg	ttc	cca	cgg	gac	ctg	aag	aag	tgc	tac	agt	gta	6432
	Gln	Glu	Glu	Pro	Leu	Phe	Pro	Arg	Asp	Leu	Lys	Lys	Cys	Tyr	Ser	Val	
	2130					2135				2140							
	gag	acc	cag	agc	tgc	agg	cgc	agg	cct	ggg	ttc	tgg	cta	gat	gaa	cag	6480
	Glu	Thr	Gln	Ser	Cys	Arg	Arg	Arg	Pro	Gly	Phe	Trp	Leu	Asp	Glu	Gln	
	2145				2150			2155					2160				

cgg aga cac tcc att gct gtc agc tgt ctg gac agc ggc tcc caa ccc 6528  
 Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro  
 2165 2170 2175

5 cgc cta tgt cca agc ccc tca agc ctg ggg ggc caa cct ctt ggg ggt 6576  
 Arg Leu Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly  
 2180 2185 2190

10 cct ggg agc cgg cct aag aaa aaa ctg agc cca ccc agt atc tct ata 6624  
 Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile  
 2195 2200 2205

15 gac ccc ccg gag agc cag ggc tct cgg ccc cca tgc agt cct ggt gtc 6672  
 Asp Pro Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val  
 2210 2215 2220

20 tgc ctg agg agg agg gcg ccg gcc agt gac tct aag gat ccc tcg gtc 6720  
 Cys Leu Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val  
 2225 2230 2235 2240

tcc agc ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac 6768  
 Ser Ser Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp  
 2245 2250 2255

25 acg ctg agt ctg tct ggt ttg tct tct gac cca aca gac atg gac ccc 6816  
 Thr Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Thr Asp Met Asp Pro  
 2260 2265 2270

30 <210> 8  
 <211> 6741  
 <212> DNA  
 <213> Rattus sp.

35 <220>  
 <221> CDS  
 <222> (1)...(6741)

40 <400> 8  
 atg gac gag gag gag gat gga gcg ggc gcc gag gag tcg gga cag ccc 48  
 Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro  
 1 5 10 15

45 cgt agc ttc acg cag ctg aac gac ctg tcc ggg gcc ggg ggc cgg cag 96  
 Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln  
 20 25 30

50 ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144  
 Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala  
 35 40 45

55 gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192  
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu  
 50 55 60

agc cag gac agc cgc ccg cgg agc tgg tgt ctg cgc acg gtc tgt aac 240  
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn  
 65 70 75 80

60 ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctg aac tgt gtg 288  
 Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val  
 85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336

	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Ile	Ala	Cys	Asp	Ser	Gln	
				100					105					110			
5	cgc	tgc	cgg	atc	ctg	cag	gcc	ttc	gat	gac	ttc	atc	ttt	gcc	ttc	ttt	384
	Arg	Cys	Arg	Ile	Leu	Gln	Ala	Phe	Asp	Asp	Phe	Ile	Phe	Ala	Phe	Phe	
			115					120					125				
10	gct	gtg	gaa	atg	gtg	gtg	aag	atg	gtg	gcc	ttg	ggc	atc	ttt	ggg	aag	432
	Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	
			130				135					140					
15	aaa	tgt	tac	ctg	gga	gac	act	tgg	aac	cgg	ctt	gac	ttt	ttc	att	gtc	480
	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val	
	145					150					155					160	
20	att	gca	ggg	atg	ctg	gag	tat	tcg	ctg	gac	ctg	cag	aac	gtc	agc	ttc	528
	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe	
					165					170					175		
25	tcc	gca	gtc	agg	aca	gtc	cgt	gtg	ctg	cga	ccg	ctc	agg	gcc	att	aac	576
	Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn	
				180					185					190			
30	cgg	gtg	ccc	agc	atg	cgc	att	ctc	gtc	aca	tta	ctg	ctg	gac	acc	ttg	624
	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu	
			195					200					205				
35	cct	atg	ctg	ggc	aac	gtc	ctg	ctc	tgt	ttc	ttc	gtc	ttt	ttc	atc	672	
	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile		
		210					215					220					
40	ttt	ggc	atc	gtg	ggc	gtc	cag	ctg	tgg	gca	gga	ctg	ctt	cgc	aac	cgg	720
	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	
	225					230					235					240	
45	tgc	ttc	ctc	ccc	gag	aac	ttc	agc	ctc	ccc	ctg	agc	gtg	gac	ctg	gag	768
	Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu	
					245					250					255		
50	cct	tat	tac	cag	aca	gag	aat	gag	gac	gag	agc	ccc	ttc	atc	tgc	tct	816
	Pro	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser	
				260					265					270			
55	cag	cct	cgg	gag	aat	ggc	atg	aga	tcc	tgc	agg	agt	gtg	ccc	aca	ctg	864
	Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu	
			275					280					285				
60	cgt	ggg	gaa	ggc	ggt	ggt	ggc	cca	ccc	tgc	agt	ctg	gac	tat	gag	acc	912
	Arg	Gly	Glu	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Ser	Leu	Asp	Tyr	Glu	Thr	
		290					295					300					
65	tat	aac	agt	tcc	agc	aac	acc	acc	tgt	gtc	aac	tgg	aac	cag	tac	tat	960
	Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr	
	305					310					315					320	
70	acc	aac	tgc	tct	gcg	ggc	gag	cac	aac	ccc	ttc	aaa	ggc	gcc	atc	aac	1008
	Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn	
					325					330					335		
75	ttt	gac	aac	att	ggc	tat	gcc	tgg	atc	gcc	atc	ttc	cag	gtc	atc	aca	1056
	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr	
				340					345					350			
80	ctg	gag	ggc	tgg	gtc	gac	atc	atg	tac	ttc	gta	atg	gac	gct	cac	tcc	1104

	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser	
			355					360					365				
5	ttc	tac	aac	ttc	atc	tac	ttc	att	ctt	ctc	atc	atc	gtg	ggc	tcc	ttc	1152
	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe	
		370					375					380					
10	ttc	atg	atc	aac	ctg	tgc	ctg	gtg	gtg	att	gcc	acg	cag	ttc	tcc	gag	1200
	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu	
		385				390					395					400	
15	acc	aaa	cag	cgg	gag	agt	cag	ctg	atg	cgg	gag	cag	cgt	gta	cga	ttc	1248
	Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe	
					405					410					415		
	ctg	tcc	aat	gct	agc	acc	ctg	gca	agc	ttc	tct	gag	cca	ggc	agc	tgc	1296
	Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys	
				420					425					430			
20	tat	gag	gag	cta	ctc	aag	tac	ctg	gtg	tac	atc	ctc	cga	aaa	gca	gcc	1344
	Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala	
			435					440					445				
25	cga	agg	ctg	gcc	cag	gtc	tct	agg	gct	ata	ggc	gtg	cgg	gct	ggg	ctg	1392
	Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ile	Gly	Val	Arg	Ala	Gly	Leu	
		450					455					460					
30	ctc	agc	agc	cca	gtg	gcc	cgt	agt	ggg	cag	gag	ccc	cag	ccc	agt	ggc	1440
	Leu	Ser	Ser	Pro	Val	Ala	Arg	Ser	Gly	Gln	Glu	Pro	Gln	Pro	Ser	Gly	
		465				470					475					480	
	agc	tgc	act	cgc	tca	cac	cgt	cgt	ctg	tct	gtc	cac	cac	ctg	gtc	cac	1488
	Ser	Cys	Thr	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His	
					485					490					495		
35	cac	cat	cac	cac	cac	cat	cac	cac	tac	cac	ctg	ggt	aat	ggg	acg	ctc	1536
	His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu	
					500				505					510			
40	aga	gtt	ccc	cgg	gcc	agc	cca	gag	atc	cag	gac	agg	gat	gcc	aat	ggg	1584
	Arg	Val	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly	
			515					520					525				
45	tct	cgc	cgg	ctc	atg	cta	cca	cca	ccc	tct	aca	ccc	act	ccc	tct	ggg	1632
	Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr	Pro	Thr	Pro	Ser	Gly	
		530					535					540					
50	ggc	cct	ccg	agg	ggt	gcg	gag	tct	gta	cac	agc	ttc	tac	cat	gct	gac	1680
	Gly	Pro	Pro	Arg	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp	
		545				550					555					560	
	tgc	cac	ttg	gag	cca	gtc	cgt	tgc	cag	gca	ccc	cct	ccc	aga	tgc	cca	1728
	Cys	His	Leu	Glu	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Cys	Pro	
					565					570					575		
55	tcg	gag	gca	tct	ggt	agg	act	gtg	ggt	agt	ggg	aag	gtg	tac	ccc	act	1776
	Ser	Glu	Ala	Ser	Gly	Arg	Thr	Val	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr	
				580					585					590			
60	gtg	cat	acc	agc	cct	cca	cca	gag	ata	ctg	aag	gat	aaa	gca	cta	gtg	1824
	Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Ile	Leu	Lys	Asp	Lys	Ala	Leu	Val	
			595					600					605				
	gag	gtg	gcc	ccc	agc	cct	ggg	ccc	ccc	acc	ctc	acc	agc	ttc	aac	atc	1872

	Glu	Val	Ala	Pro	Ser	Pro	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Phe	Asn	Ile	
	610						615					620					
5	cca	cct	ggg	ccc	ttc	agc	tcc	atg	cac	aag	ctc	ctg	gag	aca	cag	agt	1920
	Pro	Pro	Gly	Pro	Phe	Ser	Ser	Met	His	Lys	Leu	Leu	Glu	Thr	Gln	Ser	
	625					630					635					640	
10	acg	gga	gcc	tgc	cat	agc	tcc	tgc	aaa	atc	tcc	agc	cct	tgc	tcc	aag	1968
	Thr	Gly	Ala	Cys	His	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Ser	Lys	
					645					650					655		
15	gca	gac	agt	gga	gcc	tgc	ggg	ccg	gac	agt	tgt	ccc	tac	tgt	gcc	cgg	2016
	Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pro	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg	
				660					665					670			
20	aca	gga	gca	gga	gag	cca	gag	tcc	gct	gac	cat	gtc	atg	cct	gac	tca	2064
	Thr	Gly	Ala	Gly	Glu	Pro	Glu	Ser	Ala	Asp	His	Val	Met	Pro	Asp	Ser	
				675				680					685				
25	gac	agc	gag	gct	gtg	tat	gag	ttc	aca	cag	gac	gct	cag	cac	agt	gac	2112
	Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp	
		690					695					700					
30	ctc	cgg	gat	ccc	cac	agc	cgg	cgg	cga	cag	cgg	agc	ctg	ggc	cca	gat	2160
	Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	
	705					710					715					720	
35	gca	gag	cct	agt	tct	gtg	ctg	gct	ttc	tgg	agg	ctg	atc	tgt	gac	aca	2208
	Ala	Glu	Pro	Ser	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	
					725					730					735		
40	ttc	cgg	aag	atc	gta	gat	agc	aaa	tac	ttt	ggc	cgg	gga	atc	atg	atc	2256
	Phe	Arg	Lys	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	
				740					745					750			
45	gcc	atc	ctg	gtc	aat	aca	ctc	agc	atg	ggc	atc	gag	tac	cac	gag	cag	2304
	Ala	Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	Glu	Tyr	His	Glu	Gln	
			755					760					765				
50	ccc	gag	gag	ctc	acc	aac	gcc	ctg	gaa	atc	agc	aac	atc	gtc	ttc	acc	2352
	Pro	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr	
		770					775					780					
55	agc	ctc	ttc	gcc	ttg	gag	atg	ctg	ctg	aaa	ctg	ctt	gtc	tac	ggt	ccc	2400
	Ser	Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	
	785					790				795						800	
60	ttt	ggc	tac	att	aag	aat	ccc	tac	aac	atc	ttt	gat	ggt	gtc	att	gtg	2448
	Phe	Gly	Tyr	Ile	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	
					805					810					815		
65	gtc	atc	agt	gtg	tgg	gag	att	gtg	ggc	cag	cag	gga	ggt	ggc	ctg	tcg	2496
	Val	Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser	
				820					825					830			
70	gtg	ctg	cgg	acc	ttc	cgc	ctg	atg	cgg	gtg	ctg	aag	ctg	gtg	cgc	ttc	2544
	Val	Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	
				835				840					845				
75	ctg	ccg	gcc	ctg	cag	cgc	cag	ctc	gtg	gtg	ctc	atg	aag	acc	atg	gac	2592
	Leu	Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	
		850					855					860					
80	aac	gtg	gcc	acc	ttc	tgc	atg	ctc	ctc	atg	ctg	ttc	atc	ttc	atc	ttc	2640

	Asn	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	
	865					870					875					880	
5	agc	atc	ctg	ggc	atg	cat	ctc	ttt	ggg	tgc	aag	ttc	gca	tct	gaa	cgg	2688
	Ser	Ile	Leu	Gly	Met	His	Leu	Phe	Gly	Cys	Lys	Phe	Ala	Ser	Glu	Arg	
					885					890					895		
10	gat	ggg	gac	acg	ttg	cca	gac	cgg	aag	aat	ttc	gac	tcc	ctg	ctc	tgg	2736
	Asp	Gly	Asp	Thr	Leu	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp	
				900					905					910			
15	gcc	atc	gtc	act	gtc	ttt	cag	att	ctg	act	cag	gaa	gac	tgg	aat	aaa	2784
	Ala	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Lys	
			915					920					925				
20	gtc	ctc	tac	aac	ggc	atg	gcc	tcc	aca	tcg	tct	tgg	gct	gct	ctt	tac	2832
	Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr	
			930				935					940					
25	ttc	atc	gcc	ctc	atg	act	ttt	ggc	aac	tat	gtg	ctc	ttt	aac	ctg	ctg	2880
	Phe	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	
	945					950					955					960	
30	gtg	gcc	att	ctt	gtg	gaa	gga	ttc	cag	gca	gag	gga	gat	gcc	acc	aag	2928
	Val	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Gly	Asp	Ala	Thr	Lys	
					965					970					975		
35	tct	gag	tca	gag	cct	gat	ttc	ttt	tcg	ccc	agt	gtg	gat	ggt	gat	ggg	2976
	Ser	Glu	Ser	Glu	Pro	Asp	Phe	Phe	Ser	Pro	Ser	Val	Asp	Gly	Asp	Gly	
				980					985					990			
40	gac	aga	aag	aag	cgc	ttg	gcc	ctg	gtg	gct	ttg	gga	gaa	cac	gcg	gaa	3024
	Asp	Arg	Lys	Lys	Arg	Leu	Ala	Leu	Val	Ala	Leu	Gly	Glu	His	Ala	Glu	
			995					1000					1005				
45	cta	cga	aag	agc	ctt	ttg	cca	ccc	ctc	atc	atc	cat	acg	gct	gcg	aca	3072
	Leu	Arg	Lys	Ser	Leu	Leu	Pro	Pro	Leu	Ile	Ile	His	Thr	Ala	Ala	Thr	
		1010					1015					1020					
50	cca	atg	tca	cac	ccc	aag	agc	tcc	agc	aca	ggt	gtg	ggg	gaa	gca	ctg	3120
	Pro	Met	Ser	His	Pro	Lys	Ser	Ser	Ser	Thr	Gly	Val	Gly	Glu	Ala	Leu	
	1025					1030					1035					1040	
55	ggc	tct	ggc	tct	cga	cgt	acc	agt	agc	agt	ggg	tcc	gct	gag	cct	gga	3168
	Gly	Ser	Gly	Ser	Arg	Arg	Thr	Ser	Ser	Ser	Gly	Ser	Ala	Glu	Pro	Gly	
					1045					1050					1055		
60	gct	gcc	cac	cat	gag	atg	aaa	tgt	ccg	cca	agt	gcc	cgc	agc	tcc	ccg	3216
	Ala	Ala	His	His	Glu	Met	Lys	Cys	Pro	Pro	Ser	Ala	Arg	Ser	Ser	Pro	
				1060					1065					1070			
65	cac	agt	ccc	tgg	agt	gcg	gca	agc	agc	tgg	acc	agc	agg	cgc	tcc	agc	3264
	His	Ser	Pro	Trp	Ser	Ala	Ala	Ser	Ser	Trp	Thr	Ser	Arg	Arg	Ser	Ser	
			1075					1080					1085				
70	agg	aac	agc	ctg	ggc	cgg	gcc	ccc	agc	cta	aag	cgg	agg	agc	ccg	agc	3312
	Arg	Asn	Ser	Leu	Gly	Arg	Ala	Pro	Ser	Leu	Lys	Arg	Arg	Ser	Pro	Ser	
		1090					1095					1100					
75	ggg	gag	cgg	agg	tcc	ctg	ctg	tct	gga	gag	ggc	cag	gag	agt	cag	gat	3360
	Gly	Glu	Arg	Arg	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gln	Glu	Ser	Gln	Asp	
	1105					1110					1115					1120	
80	gag	gag	gaa	agt	tca	gaa	gag	gac	cgg	gcc	agc	cca	gca	ggc	agt	gac	3408

	Glu	Glu	Glu	Ser	Ser	Glu	Glu	Asp	Arg	Ala	Ser	Pro	Ala	Gly	Ser	Asp	
					1125					1130					1135		
5	cat	cgc	cac	agg	ggc	tcc	ttg	gaa	cgt	gag	gcc	aag	agt	tcc	ttt	gac	3456
	His	Arg	His	Arg	Gly	Ser	Leu	Glu	Arg	Glu	Ala	Lys	Ser	Ser	Phe	Asp	
					1140				1145					1150			
10	ctg	cct	gac	act	ctg	cag	gtg	ccg	ggg	ctg	cac	cgc	aca	gcc	agc	ggc	3504
	Leu	Pro	Asp	Thr	Leu	Gln	Val	Pro	Gly	Leu	His	Arg	Thr	Ala	Ser	Gly	
					1155			1160					1165				
15	cgg	agc	tct	gcc	tct	gag	cac	caa	gac	tgt	aat	ggc	aag	tcg	gct	tca	3552
	Arg	Ser	Ser	Ala	Ser	Glu	His	Gln	Asp	Cys	Asn	Gly	Lys	Ser	Ala	Ser	
					1170			1175				1180					
20	ggg	cgt	ttg	gcc	cgc	acc	ctg	agg	act	gat	gac	ccc	caa	ctg	gat	ggg	3600
	Gly	Arg	Leu	Ala	Arg	Leu	Arg	Thr	Asp	Asp	Pro	Gln	Leu	Asp	Gly		
					1185		1190				1195					1200	
25	gat	gat	gac	aat	gat	gag	gga	aat	ctg	agc	aaa	ggg	gaa	cgc	ata	caa	3648
	Asp	Asp	Asp	Asn	Asp	Glu	Gly	Asn	Leu	Ser	Lys	Gly	Glu	Arg	Ile	Gln	
					1205				1210						1215		
30	gcc	tgg	gtc	aga	tcc	cgg	ctt	cct	gcc	tgt	tgc	cga	gag	cga	gat	tcc	3696
	Ala	Trp	Val	Arg	Ser	Arg	Leu	Pro	Ala	Cys	Cys	Arg	Glu	Arg	Asp	Ser	
					1220				1225					1230			
35	tgg	tcg	gcc	tat	atc	ttt	cct	cct	cag	tca	agg	ttt	cgt	ctc	ctg	tgt	3744
	Trp	Ser	Ala	Tyr	Ile	Phe	Pro	Pro	Gln	Ser	Arg	Phe	Arg	Leu	Leu	Cys	
					1235			1240					1245				
40	cac	cgg	atc	atc	acc	cac	aag	atg	ttt	gac	cat	gtg	gtc	ctc	gtc	atc	3792
	His	Arg	Ile	Ile	Thr	His	Lys	Met	Phe	Asp	His	Val	Val	Leu	Val	Ile	
					1250			1255				1260					
45	atc	ttc	ctc	aac	tgt	atc	acc	atc	gct	atg	gag	cgc	ccc	aaa	att	gac	3840
	Ile	Phe	Leu	Asn	Cys	Ile	Thr	Ile	Ala	Met	Glu	Arg	Pro	Lys	Ile	Asp	
					1265		1270				1275					1280	
50	ccc	cac	agc	gct	gag	cgc	atc	ttc	ctg	acc	ctc	tcc	aac	tac	atc	ttc	3888
	Pro	His	Ser	Ala	Glu	Arg	Ile	Phe	Leu	Thr	Leu	Ser	Asn	Tyr	Ile	Phe	
					1285				1290						1295		
55	acg	gca	gtc	ttt	cta	gct	gaa	atg	aca	gtg	aag	gtg	gtg	gca	ctg	ggc	3936
	Thr	Ala	Val	Phe	Leu	Ala	Glu	Met	Thr	Val	Lys	Val	Val	Ala	Leu	Gly	
					1300			1305						1310			
60	tgg	tgc	ttt	ggg	gag	cag	gcc	tac	ctg	cgc	agc	agc	tgg	aat	gtg	ctg	3984
	Trp	Cys	Phe	Gly	Glu	Gln	Ala	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	Val	Leu	
					1315			1320					1325				
65	gac	ggc	ttg	ctg	gtg	ctc	atc	tcc	gtc	atc	gac	atc	ctg	gtc	tcc	atg	4032
	Asp	Gly	Leu	Leu	Val	Leu	Ile	Ser	Val	Ile	Asp	Ile	Leu	Val	Ser	Met	
					1330		1335				1340						
70	gtc	tcc	gac	agc	ggc	acc	aag	atc	ctt	ggc	atg	ctg	agg	gtg	ctg	cgg	4080
	Val	Ser	Asp	Ser	Gly	Thr	Lys	Ile	Leu	Gly	Met	Leu	Arg	Val	Leu	Arg	
					1345		1350				1355					1360	
75	ctg	ctg	cgg	acc	ctg	cgt	cca	ctc	agg	gtc	atc	agc	cgg	gcc	cag	gga	4128
	Leu	Leu	Arg	Thr	Leu	Arg	Pro	Leu	Arg	Val	Ile	Ser	Arg	Ala	Gln	Gly	
					1365				1370						1375		
80	ctg	aag	ctg	gtg	gta	gag	act	ctg	atg	tca	tcc	ctc	aaa	ccc	att	ggc	4176

	Leu	Lys	Leu	Val	Val	Glu	Thr	Leu	Met	Ser	Ser	Leu	Lys	Pro	Ile	Gly	
				1380					1385					1390			
5	aac	att	gtg	gtc	att	tgc	tgt	gcc	ttc	ttc	atc	att	ttt	gga	att	ctc	4224
	Asn	Ile	Val	Val	Ile	Cys	Cys	Ala	Phe	Phe	Ile	Ile	Phe	Gly	Ile	Leu	
			1395					1400					1405				
10	ggg	gtg	cag	ctc	ttc	aaa	ggg	aag	ttc	ttc	gtg	tgt	cag	ggt	gag	gac	4272
	Gly	Val	Gln	Leu	Phe	Lys	Gly	Lys	Phe	Phe	Val	Cys	Gln	Gly	Glu	Asp	
		1410					1415					1420					
15	acc	agg	aac	atc	act	aac	aaa	tcc	gac	tgc	gct	gag	gcc	agc	tac	cga	4320
	Thr	Arg	Asn	Ile	Thr	Asn	Lys	Ser	Asp	Cys	Ala	Glu	Ala	Ser	Tyr	Arg	
	1425					1430					1435					1440	
20	tgg	gtc	cgg	cac	aag	tac	aac	ttt	gac	aac	ctg	ggc	cag	gct	ctg	atg	4368
	Trp	Val	Arg	His	Lys	Tyr	Asn	Phe	Asp	Asn	Leu	Gly	Gln	Ala	Leu	Met	
					1445					1450					1455		
25	tcc	ctg	ttt	gtg	ctg	gcc	tcc	aag	gat	ggg	tgg	gtt	gac	atc	atg	tat	4416
	Ser	Leu	Phe	Val	Leu	Ala	Ser	Lys	Asp	Gly	Trp	Val	Asp	Ile	Met	Tyr	
				1460				1465					1470				
30	gat	ggg	ctg	gat	gct	gtg	ggg	gtg	gat	cag	cag	ccc	atc	atg	aac	cac	4464
	Asp	Gly	Leu	Asp	Ala	Val	Gly	Val	Asp	Gln	Gln	Pro	Ile	Met	Asn	His	
		1475					1480						1485				
35	aac	ccc	tgg	atg	ctg	cta	tac	ttc	atc	tcc	ttc	ctc	ctc	atc	gtg	gcc	4512
	Asn	Pro	Trp	Met	Leu	Leu	Tyr	Phe	Ile	Ser	Phe	Leu	Leu	Ile	Val	Ala	
		1490					1495					1500					
40	ttc	ttt	gtc	ctg	aac	atg	ttt	gtg	ggc	gtg	gtg	gtg	gag	aac	ttc	cat	4560
	Phe	Phe	Val	Leu	Asn	Met	Phe	Val	Gly	Val	Val	Val	Glu	Asn	Phe	His	
	1505					1510					1515				1520		
45	aag	tgc	aga	cag	cac	cag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	4608
	Lys	Cys	Arg	Gln	His	Gln	Glu	Glu	Glu	Glu	Glu	Ala	Arg	Arg	Arg	Glu	
					1525					1530					1535		
50	aag	cga	cta	cgg	agg	ctg	gag	aaa	aag	aga	agg	aaa	gcc	cag	tgc	aag	4656
	Lys	Arg	Leu	Arg	Arg	Leu	Glu	Lys	Lys	Arg	Arg	Lys	Ala	Gln	Cys	Lys	
				1540				1545					1550				
55	ccc	tac	tac	tct	gac	tac	tgc	aga	ttc	cgg	ctc	ctt	gtc	cac	cac	ctg	4704
	Pro	Tyr	Tyr	Ser	Asp	Tyr	Ser	Arg	Phe	Arg	Leu	Leu	Val	His	His	Leu	
		1555						1560					1565				
60	tgt	acc	agc	cac	tac	ctg	gac	ctc	ttc	atc	act	ggg	gtc	atc	ggg	ctg	4752
	Cys	Thr	Ser	His	Tyr	Leu	Asp	Leu	Phe	Ile	Thr	Gly	Val	Ile	Gly	Leu	
		1570					1575					1580					
65	aac	gtg	gtc	act	atg	gcc	atg	gaa	cat	tac	cag	cag	ccc	cag	atc	ctg	4800
	Asn	Val	Val	Thr	Met	Ala	Met	Glu	His	Tyr	Gln	Gln	Pro	Gln	Ile	Leu	
	1585					1590					1595				1600		
70	gac	gag	gct	ctg	aag	atc	tgc	aat	tac	atc	ttt	acc	gtc	atc	ttt	gtc	4848
	Asp	Glu	Ala	Leu	Lys	Ile	Cys	Asn	Tyr	Ile	Phe	Thr	Val	Ile	Phe	Val	
				1605					1610						1615		
75	ttt	gag	tca	gtt	ttc	aaa	ctt	gtg	gcc	ttt	ggc	ttc	cgc	cgt	ttc	ttc	4896
	Phe	Glu	Ser	Val	Phe	Lys	Leu	Val	Ala	Phe	Gly	Phe	Arg	Arg	Phe	Phe	
				1620					1625					1630			
80	cag	gac	agg	tgg	aac	cag	ctg	gac	ctg	gct	att	gtg	ctt	ctg	tcc	atc	4944



	Gln	Asp	Arg	Trp	Asn	Gln	Leu	Asp	Leu	Ala	Ile	Val	Leu	Leu	Ser	Ile	
			1635					1640					1645				
5	arg	ggc	atc	aca	ctg	gag	gag	att	gag	gtc	aac	ctg	tgc	ctg	ccc	atc	4992
	Met	Gly	Ile	Thr	Leu	Glu	Glu	Ile	Glu	Val	Asn	Leu	Ser	Leu	Pro	Ile	
		1650				1655					1660						
10	aac	ccc	acc	atc	atc	cgt	atc	atg	agg	gtg	ctc	cgc	att	gct	cga	gtt	5040
	Asn	Pro	Thr	Ile	Ile	Arg	Ile	Met	Arg	Val	Leu	Arg	Ile	Ala	Arg	Val	
	1665				1670					1675					1680		
15	ctg	aag	ctg	ttg	aag	atg	gct	gtg	ggc	atg	cgg	gca	ctg	ctg	cac	acg	5088
	Leu	Lys	Leu	Leu	Lys	Met	Ala	Val	Gly	Met	Arg	Ala	Leu	Leu	His	Thr	
				1685					1690						1695		
20	gtg	atg	cag	gcc	ctg	ccc	cag	gtg	ggg	aac	ctg	gga	ctt	ctc	ttc	atg	5136
	Val	Met	Gln	Ala	Leu	Pro	Gln	Val	Gly	Asn	Leu	Gly	Leu	Leu	Phe	Met	
			1700					1705					1710				
25	tta	ttg	ttt	ttc	atc	ttt	gca	gct	ctg	ggc	gtg	gag	ctc	ttt	gga	gac	5184
	Leu	Leu	Phe	Phe	Ile	Phe	Ala	Ala	Leu	Gly	Val	Glu	Leu	Phe	Gly	Asp	
		1715					1720					1725					
30	ctg	gag	tgt	gat	gag	aca	cac	cct	tgt	gag	ggc	ttg	ggt	cgg	cat	gcc	5232
	Leu	Glu	Cys	Asp	Glu	Thr	His	Pro	Cys	Glu	Gly	Leu	Gly	Arg	His	Ala	
		1730				1735				1740							
35	acc	ttt	agg	aac	ttt	ggt	atg	gcc	ttt	ctg	acc	ctc	ttc	cga	gtc	tcc	5280
	Thr	Phe	Arg	Asn	Phe	Gly	Met	Ala	Phe	Leu	Thr	Leu	Phe	Arg	Val	Ser	
	1745				1750				1755						1760		
40	act	ggt	gac	aac	tgg	aat	ggt	att	atg	aag	gac	acc	ctc	cgg	gac	tgt	5328
	Thr	Gly	Asp	Asn	Trp	Asn	Gly	Ile	Met	Lys	Asp	Thr	Leu	Arg	Asp	Cys	
				1765					1770					1775			
45	gac	cag	gag	tcc	acc	tgc	tac	aac	act	gtc	atc	tcc	cct	atc	tac	ttt	5376
	Asp	Gln	Glu	Ser	Thr	Cys	Tyr	Asn	Thr	Val	Ile	Ser	Pro	Ile	Tyr	Phe	
			1780					1785					1790				
50	gtg	tcc	ttc	gtg	ctg	acg	gcc	cag	ttt	gtg	ctg	gtc	aac	gtg	gtc	ata	5424
	Val	Ser	Phe	Val	Leu	Thr	Ala	Gln	Phe	Val	Leu	Val	Asn	Val	Val	Ile	
		1795					1800					1805					
55	gct	gtg	ctg	atg	aag	cac	ctg	gaa	gaa	agc	aac	aaa	gag	gcc	aag	gag	5472
	Ala	Val	Leu	Met	Lys	His	Leu	Glu	Glu	Ser	Asn	Lys	Glu	Ala	Lys	Glu	
		1810				1815				1820							
60	gag	gcc	gag	ctc	gag	gcc	gag	ctg	gag	ctg	gag	atg	aag	acg	ctc	agc	5520
	Glu	Ala	Glu	Leu	Glu	Ala	Glu	Leu	Glu	Leu	Glu	Met	Lys	Thr	Leu	Ser	
	1825				1830				1835						1840		
65	ccg	cag	ccc	cac	tcc	ccg	ctg	ggc	agc	ccc	ttc	ctc	tgg	ccc	ggg	gtg	5568
	Pro	Gln	Pro	His	Ser	Pro	Leu	Gly	Ser	Pro	Phe	Leu	Trp	Pro	Gly	Val	
				1845					1850					1855			
70	gag	ggt	gtc	aac	agt	act	gac	agc	cct	aag	cct	ggg	gct	cca	cac	acc	5616
	Glu	Gly	Val	Asn	Ser	Thr	Asp	Ser	Pro	Lys	Pro	Gly	Ala	Pro	His	Thr	
			1860					1865				1870					
75	act	gcc	cac	att	gga	gca	gcc	tgc	ggc	ttc	tcc	ctt	gag	cac	ccc	acg	5664
	Thr	Ala	His	Ile	Gly	Ala	Ala	Ser	Gly	Phe	Ser	Leu	Glu	His	Pro	Thr	
		1875					1880					1885					
80	atg	gta	ccc	cac	ccc	gag	gag	gtg	cca	gtc	ccc	cta	gga	cca	gac	ctg	5712

	Met	Val	Pro	His	Pro	Glu	Glu	Val	Pro	Val	Pro	Leu	Gly	Pro	Asp	Leu	
	1890					1895					1900						
5	ctg	act	gtg	agg	aag	tct	ggt	gtc	agc	cgg	acg	cac	tct	ctg	ccc	aat	5760
	Leu	Thr	Val	Arg	Lys	Ser	Gly	Val	Ser	Arg	Thr	His	Ser	Leu	Pro	Asn	
	1905				1910					1915						1920	
10	gac	agc	tac	atg	tgc	cgc	aat	ggg	agc	act	gct	gag	aga	tcc	cta	gga	5808
	Asp	Ser	Tyr	Met	Cys	Arg	Asn	Gly	Ser	Thr	Ala	Glu	Arg	Ser	Leu	Gly	
				1925					1930						1935		
15	cac	agg	ggc	tgg	ggg	ctc	ccc	aaa	gcc	cag	tca	ggc	tcc	atc	ttg	tcc	5856
	His	Arg	Gly	Trp	Gly	Leu	Pro	Lys	Ala	Gln	Ser	Gly	Ser	Ile	Leu	Ser	
			1940					1945					1950				
20	gtt	cac	tcc	caa	cca	gca	gac	acc	agc	tgc	atc	cta	cag	ctt	ccc	aaa	5904
	Val	His	Ser	Gln	Pro	Ala	Asp	Thr	Ser	Cys	Ile	Leu	Gln	Leu	Pro	Lys	
			1955				1960						1965				
25	gat	gtg	cac	tat	ctg	ctc	cag	cct	cat	ggg	gct	ccc	acc	tgg	ggc	gcc	5952
	Asp	Val	His	Tyr	Leu	Leu	Gln	Pro	His	Gly	Ala	Pro	Thr	Trp	Gly	Ala	
	1970				1975							1980					
30	atc	cct	aaa	cta	ccc	cca	cct	ggc	cgc	tcc	cct	ctg	gct	cag	agg	cct	6000
	Ile	Pro	Lys	Leu	Pro	Pro	Pro	Gly	Arg	Ser	Pro	Leu	Ala	Gln	Arg	Pro	
	1985				1990					1995						2000	
35	ctc	agg	cgc	cag	gca	gca	ata	agg	act	gac	tcc	ctg	gat	gtg	cag	ggc	6048
	Leu	Arg	Arg	Gln	Ala	Ala	Ile	Arg	Thr	Asp	Ser	Leu	Asp	Val	Gln	Gly	
				2005					2010					2015			
40	ctg	ggt	agc	cgg	gaa	gac	ctg	ttg	tca	gag	gtg	agt	ggg	ccc	tcc	tgc	6096
	Leu	Gly	Ser	Arg	Glu	Asp	Leu	Leu	Ser	Glu	Val	Ser	Gly	Pro	Ser	Cys	
				2020				2025					2030				
45	cct	ctg	acc	cgg	tcc	tca	tcc	ttc	tgg	ggc	ggg	tgc	agc	atc	cag	gtg	6144
	Pro	Leu	Thr	Arg	Ser	Ser	Ser	Phe	Trp	Gly	Gly	Ser	Ser	Ile	Gln	Val	
			2035				2040					2045					
50	cag	cag	cgt	tcc	ggc	atc	cag	agc	aaa	gtc	tcc	aag	cac	atc	cgc	ctg	6192
	Gln	Gln	Arg	Ser	Gly	Ile	Gln	Ser	Lys	Val	Ser	Lys	His	Ile	Arg	Leu	
	2050				2055						2060						
55	cca	gcc	cct	tgc	cca	ggc	ctg	gaa	ccc	agc	tgg	gcc	aag	gac	cct	cca	6240
	Pro	Ala	Pro	Cys	Pro	Gly	Leu	Glu	Pro	Ser	Trp	Ala	Lys	Asp	Pro	Pro	
	2065				2070				2075						2080		
60	gag	acc	aga	agc	agc	tta	gag	ctg	gac	acg	gag	ctg	agc	tgg	att	tca	6288
	Glu	Thr	Arg	Ser	Ser	Leu	Glu	Leu	Asp	Thr	Glu	Leu	Ser	Trp	Ile	Ser	
				2085				2090					2095				
65	gga	gac	ctc	ctt	ccc	agc	agc	cag	gaa	gaa	ccc	ctg	ttc	cca	cgg	gac	6336
	Gly	Asp	Leu	Leu	Pro	Ser	Ser	Gln	Glu	Glu	Pro	Leu	Phe	Pro	Arg	Asp	
			2100					2105				2110					
70	ctg	aag	aag	tgc	tac	agt	gta	gag	acc	cag	agc	tgc	agg	cgc	agg	cct	6384
	Leu	Lys	Lys	Cys	Tyr	Ser	Val	Glu	Thr	Gln	Ser	Cys	Arg	Arg	Arg	Pro	
		2115					2120					2125					
75	ggg	ttc	tgg	cta	gat	gaa	cag	cgg	aga	cac	tcc	att	gct	gtc	agc	tgt	6432
	Gly	Phe	Trp	Leu	Asp	Glu	Gln	Arg	Arg	His	Ser	Ile	Ala	Val	Ser	Cys	
	2130					2135					2140						
80	ctg	gac	agc	ggc	tcc	caa	ccc	cgc	cta	tgt	cca	agc	ccc	tca	agc	ctc	6480

	Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser Ser Leu	
	2145 2150 2155 2160	
5	ggg ggc caa cct ctt ggg ggt cct ggg agc cgg cct aag aaa aaa ctc Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu	6528
	2165 2170 2175	
10	agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc tct cgg Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly Ser Arg	6576
	2180 2185 2190	
15	ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg gcc agt Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro Ala Ser	6624
	2195 2200 2205	
	gac tct aag gat ccc tgc gtc tcc agc ccc ctt gac agc acg gct gcc Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr Ala Ala	6672
	2210 2215 2220	
20	tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg tct tct Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu Ser Ser	6720
	2225 2230 2235 2240	
25	gac cca aca gac atg gac ccc Asp Pro Thr Asp Met Asp Pro	6741
	2245	
30	<210> 9 <211> 6132 <212> DNA <213> Homo sapiens	
35	<220> <221> CDS <222> (1)..(6132)	
40	<400> 9 atg acc gag ggc gca cgg gcc gcc gac gag gtc cgg gtg ccc ctg ggg Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly	48
	1 5 10 15	
45	cgc cgc ccc tgg ccc tgc ggc gtt ggt ggg ggc gtc ccc gga gag ccc Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Val Pro Gly Glu Pro	96
	20 25 30	
50	cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca Arg Gly Ala Gly Thr Arg Gly Gly Gly Phe Glu Leu Gly Val Ser	144
	35 40 45	
	ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp	192
	50 55 60	
55	gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Thr Val Phe Phe	240
	65 70 75 80	
60	tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val	288
	85 90 95	
	tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn	336

	100								105								110								
5	tgc	gtg	acc	ctg	ggc	atg	ttc	cgg	ccc	tgt	gag	gac	gtt	gag	tgc	ggc									384
	Cys	Val	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Val	Glu	Cys	Gly									
			115					120					125												
10	tcc	gag	cgc	tgc	aac	atc	ctg	gag	gcc	ttt	gac	gcc	ttc	att	ttc	gcc									432
	Ser	Glu	Arg	Cys	Asn	Ile	Leu	Glu	Ala	Phe	Asp	Ala	Phe	Ile	Phe	Ala									
			130				135					140													
15	ttt	ttt	gcg	gtg	gag	atg	gtc	atc	aag	atg	gtg	gcc	ttg	ggg	ctg	ttc									480
	Phe	Phe	Ala	Val	Glu	Met	Val	Ile	Lys	Met	Val	Ala	Leu	Gly	Leu	Phe									
			145			150					155					160									
20	ggg	cag	aag	tgt	tac	ctg	ggt	gac	acg	tgg	aac	agg	ctg	gat	ttc	ttc									528
	Gly	Gln	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe									
					165					170					175										
25	atc	gtc	gtg	gcg	ggc	atg	atg	gag	tac	tgc	ttg	gac	gga	cac	aac	gtg									576
	Ile	Val	Val	Ala	Gly	Met	Met	Glu	Tyr	Ser	Leu	Asp	Gly	His	Asn	Val									
				180					185					190											
30	agc	ctc	tgc	gct	atc	agg	acc	gtg	cgg	gtg	ctg	cgg	ccc	ctc	cgc	gcc									624
	Ser	Leu	Ser	Ala	Ile	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala									
			195					200					205												
35	atc	aac	cgc	gtg	cct	agc	atg	cgg	atc	ctg	gtc	act	ctg	ctg	ctg	gat									672
	Ile	Asn	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp									
			210				215					220													
40	acg	ctg	ccc	atg	ctc	ggg	aac	gtc	ctt	ctg	ctg	tgc	ttc	ttc	gtc	ttc									720
	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe									
			225			230					235					240									
45	ttc	att	ttc	ggc	atc	gtt	ggc	gtc	cag	ctc	tgg	gct	ggc	ctc	ctg	cgg									768
	Phe	Ile	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg									
				245						250					255										
50	aac	cgc	tgc	ttc	ctg	gac	agt	gcc	ttt	gtc	agg	aac	aac	aac	ctg	acc									816
	Asn	Arg	Cys	Phe	Leu	Asp	Ser	Ala	Phe	Val	Arg	Asn	Asn	Asn	Leu	Thr									
				260				265					270												
55	ttc	ctg	cgg	ccg	tac	tac	cag	acg	gag	gag	ggc	gag	gag	aac	ccg	ttc									864
	Phe	Leu	Arg	Pro	Tyr	Tyr	Gln	Thr	Glu	Glu	Gly	Glu	Glu	Asn	Pro	Phe									
			275					280					285												
60	atc	tgc	tcc	tca	cgc	cga	gac	aac	ggc	atg	cag	aag	tgc	tgc	cac	atc									912
	Ile	Cys	Ser	Ser	Arg	Arg	Asp	Asn	Gly	Met	Gln	Lys	Cys	Ser	His	Ile									
			290				295					300													
65	ccc	ggc	cgc	cgc	gac	gtg	cgc	atg	ccc	tgc	acc	ctg	ggc	tgg	gag	gcc									960
	Pro	Gly	Arg	Arg	Asp	Val	Arg	Met	Pro	Cys	Thr	Leu	Gly	Trp	Glu	Ala									
			305			310					315					320									
70	tac	acg	cag	ccg	cag	gcc	gag	ggg	gtg	ggc	gct	gca	cgc	aac	gcc	tgc									1008
	Tyr	Thr	Gln	Pro	Gln	Ala	Glu	Gly	Val	Gly	Ala	Ala	Arg	Asn	Ala	Cys									
				325				330							335										
75	atc	aac	tgg	aac	cag	tac	tac	aac	gtg	tgc	cgc	tgc	ggt	gac	tcc	aac									1056
	Ile	Asn	Trp	Asn	Gln	Tyr	Tyr	Asn	Val	Cys	Arg	Ser	Gly	Asp	Ser	Asn									
				340				345						350											
80	ccc	cac	aac	ggt	gcc	atc	aac	ttc	gac	aac	acc	tgc	tac	gcc	tgg	att									1104
	Pro	His	Asn	Gly	Ala	Ile	Asn	Phe	Asp	Asn	Thr	Cys	Tyr	Ala	Trp	Ile									

	355	360	365	
5	gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac atc atg tac Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr 370 375 380	1152		
10	tac gtc atg gac gcc cac tca ttc tac aac ttc atc tat ttc atc ctg Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu 385 390 395 400	1200		
15	ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val 405 410 415	1248		
20	att gcc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met 420 425 430	1296		
25	cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser 435 440 445	1344		
30	ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly 450 455 460	1392		
35	cac ata ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg 465 470 475 480	1440		
40	tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly 485 490 495	1488		
45	cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser 500 505 510	1536		
50	gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac tac Val His His Leu Val Tyr His His His His His His His His His Tyr 515 520 525	1584		
55	cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala 530 535 540	1632		
60	tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser 545 550 555 560	1680		
65	cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His 565 570 575	1728		
70	gcc gac tgc cac ata gag ggg cgg cag gag agg gcc cgg gtg ggc aca Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr 580 585 590	1776		
75	tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly 595 600 605	1824		
80	cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln 610 615 620	1872		

	610	615	620	
5	agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala 625 630 635 640			1920
10	agg cac cgg ggg cac ggc cgg ttg agc ttg aac agc cct gat ccc tac Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr 645 650 655			1968
15	gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro 660 665 670			2016
20	ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro 675 680 685			2064
25	gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg 690 695 700			2112
30	gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp 705 710 715 720			2160
35	tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly 725 730 735			2208
40	gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly 740 745 750			2256
45	cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro 755 760 765			2304
50	ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys 770 775 780			2352
55	ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met 785 790 795 800			2400
60	gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln 805 810 815			2448
65	ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr 820 825 830			2496
70	agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro 835 840 845			2544
75	ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val 850 855 860			2592
80	gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser 865 870 875			2640

	865		870		875		880	
5	gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttc							2688
	Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe							
			885				890	895
10	ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac							2736
	Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp							
			900				905	910
15	aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc							2784
	Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe							
			915				920	925
20	agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca							2832
	Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr							
			930				935	940
25	gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg							2880
	Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu							
			945				950	955
30	tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac							2928
	Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn							
			965				970	975
35	gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc							2976
	Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu							
			980				985	990
40	tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg							3024
	Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu							
			995			1000	1005	
45	ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac							3072
	Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn							
			1010			1015	1020	
50	aga tcc gac acg gac gag gac aag acg tgc gtc cac ttc gag gag gac							3120
	Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp							
			1025			1030	1035	1040
55	ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc							3168
	Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser							
			1045			1050	1055	
60	ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc							3216
	Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro							
			1060			1065	1070	
65	ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga							3264
	Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg							
			1075			1080	1085	
70	gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg							3312
	Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val							
			1090			1095	1100	
75	gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg							3360
	Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg							
			1105			1110	1115	1120
80	cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg							3408
	Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp							

	1125	1130	1135	
5	agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln 1140 1145 1150			3456
10	gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu 1155 1160 1165			3504
15	ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser 1170 1175 1180			3552
20	ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg 1185 1190 1195 1200			3600
25	ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly 1205 1210 1215			3648
30	cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His 1220 1225 1230			3696
35	cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys 1235 1240 1245			3744
40	ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg 1250 1255 1260			3792
45	agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn 1265 1270 1275 1280			3840
50	cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp 1285 1290 1295			3888
55	cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu 1300 1305 1310			3936
60	gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser 1315 1320 1325			3984
65	gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val 1330 1335 1340			4032
70	aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln 1345 1350 1355 1360			4080
75	agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val 1365 1370 1375			4128
80	gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly 1380 1385 1390 1395			4176



	1380	1385	1390	
5	gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val 1395 1400 1405	4224		
10	atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser 1410 1415 1420	4272		
15	tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe 1425 1430 1435 1440	4320		
20	atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr 1445 1450 1455	4368		
25	tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys 1460 1465 1470	4416		
30	cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn 1475 1480 1485	4464		
35	ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly 1490 1495 1500	4512		
40	tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln 1505 1510 1515 1520	4560		
45	cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser 1525 1530 1535	4608		
50	ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val 1540 1545 1550	4656		
55	gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu 1555 1560 1565	4704		
60	gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg 1570 1575 1580	4752		
65	agg agc act ttc ccc agc cca gag gcc cag cgc cgg ccc tac tat gcc Arg Ser Thr Phe Pro Ser Pro Glu Ala Gln Arg Arg Pro Tyr Tyr Ala 1585 1590 1595 1600	4800		
70	gac tac tcg ccc acg cgc cgc tgg att cac tcg ctg tgc acc agc cac Asp Tyr Ser Pro Thr Arg Arg Trp Ile His Ser Leu Cys Thr Ser His 1605 1610 1615	4848		
75	tat ctc gac ctc ttc atc acc ttc atc atc tgt gtc aac gtc atc acc Tyr Leu Asp Leu Phe Ile Thr Phe Ile Ile Cys Val Asn Val Ile Thr 1620 1625 1630	4896		
80	atg tcc atg gag cac tat aac caa ccc aag tcg ctg gac gag gcc ctc Met Ser Met Glu His Tyr Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu 1635 1640 1645 1650	4944		

	1635	1640	1645	
5	aag tac tgc aac tac gtc ttc acc atc gtg ttt gtc ttc gag gct gca Lys Tyr Cys Asn Tyr Val Phe Thr Ile Val Phe Val Phe Glu Ala Ala 1650 1655 1660			4992
10	ctg aag ctg gta gca ttt ggg ttc cgt cgg ttc ttc aag gac agg tgg Leu Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp 1665 1670 1675 1680			5040
15	aac cag ctg gac ctg gcc atc gtg ctg ctg tca ctc atg ggc atc acg Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Leu Met Gly Ile Thr 1685 1690 1695			5088
20	ctg gag gag ata gag atg agc gcc gcg ctg ccc atc aac ccc acc atc Leu Glu Glu Ile Glu Met Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile 1700 1705 1710			5136
25	atc cgc atc atg cgc gtg ctt cgc att gcc cgt gtg ctg aag ctg ctg Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu 1715 1720 1725			5184
30	aag atg gct acg ggc atg cgc gcc ctg ctg gac act gtg gtg caa gct Lys Met Ala Thr Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala 1730 1735 1740			5232
35	ctc ccc cag gtg ggg aac ctg ggc ctt ctt ttc atg ctc ctg ttt ttt Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe 1745 1750 1755 1760			5280
40	atc tat gct gcg ctg gga gtg gag ctg ttc ggg agg ctg gag tgc agt Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe Gly Arg Leu Glu Cys Ser 1765 1770 1775			5328
45	gaa gac aac ccc tgc gag ggc ctg agc agg cac gcc acc ttc agc aac Glu Asp Asn Pro Cys Glu Gly Leu Ser Arg His Ala Thr Phe Ser Asn 1780 1785 1790			5376
50	ttc ggc atg gcc ttc ctc acg ctg ttc cgc gtg tcc acg ggg gac aac Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn 1795 1800 1805			5424
55	tgg aac ggg atc atg aag gac acg ctg cgc gag tgc tcc cgt gag gac Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp 1810 1815 1820			5472
60	aag cac tgc ctg agc tac ctg ccg gcc ccg tcc ccc gtc tac ttc gtg Lys His Cys Leu Ser Tyr Leu Pro Ala Pro Ser Pro Val Tyr Phe Val 1825 1830 1835 1840			5520
65	acc ttc gtg ctg gtg ccc cag ttc gtg ctg gtg aac gtg gtg gtg gcc Thr Phe Val Leu Val Pro Gln Phe Val Leu Val Asn Val Val Val Ala 1845 1850 1855			5568
70	gtg ctc atg aag cac ctg gag gag agc aac aag gag gct cgg gag gat Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp 1860 1865 1870			5616
75	gcg gag ctg gac gcc gag atc gag ctg gag atg gcg cag ggc ccc ggg Ala Glu Leu Asp Ala Glu Ile Glu Leu Glu Met Ala Gln Gly Pro Gly 1875 1880 1885			5664
80	agt gca cgc cgg gtg gac gcg gac agg cct ccc ttg ccc cag gag agt Ser Ala Arg Arg Val Asp Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser 1890 1895 1900			5712

	1890	1895	1900	
5	ccg ggc gcc agg gac gcc cca aac ctg gtt gca cgc aag gtg tcc gtg Pro Gly Ala Arg Asp Ala Pro Asn Leu Val Ala Arg Lys Val Ser Val 1905 1910 1915 1920			5760
10	tcc agg atg ctc tcg ctg ccc aac gac agc tac atg ttc agg ccc gtg Ser Arg Met Leu Ser Leu Pro Asn Asp Ser Tyr Met Phe Arg Pro Val 1925 1930 1935			5808
	gtg cct gcc tcg gcg ccc cac ccc cgc ccg ctg cag gag gtg gag atg Val Pro Ala Ser Ala Pro His Pro Arg Pro Leu Gln Glu Val Glu Met 1940 1945 1950			5856
15	gag acc tat ggg gcc ggc acc ccc ttg ggc tcc gtt gcc tct gtg cac Glu Thr Tyr Gly Ala Gly Thr Pro Leu Gly Ser Val Ala Ser Val His 1955 1960 1965			5904
20	tct ccg ccc gca gag tcc tgt gcc tcc ctc cag atc cca ctg gct gtg Ser Pro Pro Ala Glu Ser Cys Ala Ser Leu Gln Ile Pro Leu Ala Val 1970 1975 1980			5952
25	tcg tcc cca gcc agg agc ggc gag ccc ctc cac gcc ctg tcc cct cgg Ser Ser Pro Ala Arg Ser Gly Glu Pro Leu His Ala Leu Ser Pro Arg 1985 1990 1995 2000			6000
30	ggc aca gcc cgc tcc ccc agt ctc agc cgg ctg ctc tgc aga cag gag Gly Thr Ala Arg Ser Pro Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu 2005 2010 2015			6048
	gct gtg cac acc gat tcc ttg aag gga aga ttg aca gcc cta ggg aca Ala Val His Thr Asp Ser Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr 2020 2025 2030			6096
35	ccc tgg atc ctg cag agc ctg gtg aga aaa ccc cgg Pro Trp Ile Leu Gln Ser Leu Val Arg Lys Pro Arg 2035 2040			6132
40	<210> 10 <211> 6114 <212> DNA <213> Homo sapiens			
45	<220> <221> CDS <222> (1)..(6114)			
50	<400> 10 atg acc gag ggc gca cgg gcc gcc gac gag gtc cgg gtg ccc ctg ggg Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly 1 5 10 15			48
55	cgc cgc ccc tgg ccc tgc ggc gtt ggt ggg ggc gtc ccc gga gag ccc Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro 20 25 30			96
60	cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser 35 40 45			144
	ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp 50 55 60			192

5	gag gag cag cgc gtc cgc tac cgc gcc ttg gcg gcc acg gtc ttc ttc																240
	Glu	Glu	Gln	Arg	Val	Pro	Tyr	Pro	Ala	Leu	Ala	Ala	Thr	Val	Phe	Phe	80
10	tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc																288
	Cys	Leu	Gly	Gln	Thr	Thr	Arg	Pro	Arg	Ser	Trp	Cys	Leu	Arg	Leu	Val	95
15	tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac																336
	Cys	Asn	Pro	Trp	Phe	Glu	His	Val	Ser	Met	Leu	Val	Ile	Met	Leu	Asn	110
20	tgc gtg acc ctg ggc atg ttc cgg ccc tgt gag gac gtt gag tgc ggc																384
	Cys	Val	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Val	Glu	Cys	Gly	125
25	tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc																432
	Ser	Glu	Arg	Cys	Asn	Ile	Leu	Glu	Ala	Phe	Asp	Ala	Phe	Ile	Phe	Ala	140
30	ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc																480
	Phe	Phe	Ala	Val	Glu	Met	Val	Ile	Lys	Met	Val	Ala	Leu	Gly	Leu	Phe	155
35	ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc																528
	Gly	Gln	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	175
40	atc gtc gtg gcg ggc atg atg gag tac tgc ttg gac gga cac aac gtg																576
	Ile	Val	Val	Ala	Gly	Met	Met	Glu	Tyr	Ser	Leu	Asp	Gly	His	Asn	Val	185
45	agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc																624
	Ser	Leu	Ser	Ala	Ile	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	205
50	atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat																672
	Ile	Asn	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	220
55	acg ctg ccc atg ctc ggg aac gtc ctt ctg ctg tgc ttc ttc gtc ttc																720
	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	235
60	ttc att ttc ggc atc gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg																768
	Phe	Ile	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	245
65	aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc																816
	Asn	Arg	Cys	Phe	Leu	Asp	Ser	Ala	Phe	Val	Arg	Asn	Asn	Asn	Leu	Thr	265
70	ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc																864
	Phe	Leu	Arg	Pro	Tyr	Tyr	Gln	Thr	Glu	Glu	Gly	Glu	Glu	Asn	Pro	Phe	275
75	atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc																912
	Ile	Cys	Ser	Ser	Arg	Arg	Asp	Asn	Gly	Met	Gln	Lys	Cys	Ser	His	Ile	290
80	ccc ggc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc																960
	Pro	Gly	Arg	Arg	Asp	Val	Arg	Met	Pro	Cys	Thr	Leu	Gly	Trp	Glu	Ala	310

	tac	acg	cag	ccg	cag	gcc	gag	ggg	gtg	ggc	gct	gca	ggc	aac	gcc	tgc	1003
	Tyr	Thr	Gln	Pro	Gln	Ala	Glu	Gly	Val	Gly	Ala	Ala	Arg	Asn	Ala	Cys	
					325					330					335		
5	atc	aac	tgg	aac	cag	tac	tac	aac	gtg	tgc	cgc	tcg	ggc	gac	tcc	aac	1056
	Ile	Asn	Trp	Asn	Gln	Tyr	Tyr	Asn	Val	Cys	Arg	Ser	Gly	Asp	Ser	Asn	
				340					345					350			
10	ccc	cac	aac	ggc	gcc	atc	aac	ttc	gac	aac	acc	tgc	tac	gcc	tgg	att	1104
	Pro	His	Asn	Gly	Ala	Ile	Asn	Phe	Asp	Asn	Thr	Cys	Tyr	Ala	Trp	Ile	
			355					360					365				
15	gcc	atc	ttc	cag	gtg	atc	acg	ctg	gaa	ggc	tgg	gtg	gac	atc	atg	tac	1152
	Ala	Ile	Phe	Gln	Val	Ile	Thr	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	
		370					375					380					
20	tac	gtc	atg	gac	gcc	cac	tca	ttc	tac	aac	ttc	atc	tat	ttc	atc	ctg	1200
	Tyr	Val	Met	Asp	Ala	His	Ser	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	
	385					390					395					400	
25	ctc	atc	atc	gtg	ggc	tcc	ttc	ttc	atg	atc	aac	ctg	tgc	ctg	gtg	gtg	1248
	Leu	Ile	Ile	Val	Gly	Ser	Phe	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	
					405					410					415		
30	att	gcc	acg	cag	ttc	tcg	gag	acg	aag	cag	cgg	gag	agt	cag	ctg	atg	1296
	Ile	Ala	Thr	Gln	Phe	Ser	Glu	Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	
				420					425					430			
35	cgg	gag	cag	cgg	gca	cgc	cac	ctg	tcc	aac	gac	agc	acg	ctg	gcc	agc	1344
	Arg	Glu	Gln	Arg	Ala	Arg	His	Leu	Ser	Asn	Asp	Ser	Thr	Leu	Ala	Ser	
				435				440					445				
40	ttc	tcc	gag	cct	ggc	agc	tgc	tac	gaa	gag	ctg	ctg	aag	tac	gtg	ggc	1392
	Phe	Ser	Glu	Pro	Gly	Ser	Cys	Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Val	Gly	
		450					455					460					
45	cac	ata	ttc	cgc	aag	gtc	aag	cgg	cgc	agc	ttg	cgc	ctc	tac	gcc	cgc	1440
	His	Ile	Phe	Arg	Lys	Val	Lys	Arg	Arg	Ser	Leu	Arg	Leu	Tyr	Ala	Arg	
	465					470					475					480	
50	tgg	cag	agc	cgc	tgg	cgc	aag	aag	gtg	gac	ccc	agt	gct	gtg	caa	ggc	1488
	Trp	Gln	Ser	Arg	Trp	Arg	Lys	Lys	Val	Asp	Pro	Ser	Ala	Val	Gln	Gly	
					485					490					495		
55	cag	ggc	ccc	ggg	cac	cgc	cag	cgc	cgg	gca	ggc	agg	cac	aca	gcc	tcg	1536
	Gln	Gly	Pro	Gly	His	Arg	Gln	Arg	Arg	Ala	Gly	Arg	His	Thr	Ala	Ser	
				500					505					510			
60	gtg	cac	cac	ctg	gtc	tac	cac	cac	cat	cac	cac	cac	cac	cac	cac	tac	1584
	Val	His	His	Leu	Val	Tyr	His	His	His	His	His	His	His	His	His	Tyr	
				515				520					525				
65	cat	ttc	agc	cat	ggc	agc	ccc	cgc	agg	ccc	ggc	ccc	gag	cca	ggc	gcc	1632
	His	Phe	Ser	His	Gly	Ser	Pro	Arg	Arg	Pro	Gly	Pro	Glu	Pro	Gly	Ala	
				530			535					540					
70	tgc	gac	acc	agg	ctg	gtc	cga	gct	ggc	gcg	ccc	ccc	tcg	cca	cct	tcc	1680
	Cys	Asp	Thr	Arg	Leu	Val	Arg	Ala	Gly	Ala	Pro	Pro	Ser	Pro	Pro	Ser	
		545				550					555					560	
75	cca	ggc	cgc	gga	ccc	ccc	gac	gca	gag	tct	gtg	cac	agc	atc	tac	cat	1728
	Pro	Gly	Arg	Gly	Pro	Pro	Asp	Ala	Glu	Ser	Val	His	Ser	Ile	Tyr	His	
					565					570					575		

5	gcc gac tgc cac ata gag ggg ccg cag gag agg gcc cgg gtg ggc aca	1776
	Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr	
	580 585 590	
10	tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg	1824
	Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly	
	595 600 605	
15	cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa	1872
	His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln	
	610 615 620	
20	agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc	1920
	Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala	
	625 630 635 640	
25	agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac	1968
	Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr	
	645 650 655	
30	gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct	2016
	Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro	
	660 665 670	
35	ggc cat ctg tgc ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca	2064
	Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro	
	675 680 685	
40	gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt	2112
	Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg	
	690 695 700	
45	gcc ctg gag gac ccg gag ggt gag ctc agc ggc tgc gaa agt gga gac	2160
	Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp	
	705 710 715 720	
50	tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt	2208
	Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly	
	725 730 735	
55	gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc	2256
	Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly	
	740 745 750	
60	cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg	2304
	Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro	
	755 760 765	
65	ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag	2352
	Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys	
	770 775 780	
70	ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg	2400
	Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met	
	785 790 795 800	
75	gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag	2448
	Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln	
	805 810 815	
80	ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc	2496
	Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr	
	820 825 830	

5	agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct	2544
	Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro	
	835 840 845	
10	ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg	2592
	Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val	
	850 855 860	
15	gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct	2640
	Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser	
	865 870 875 880	
20	gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttc	2688
	Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe	
	885 890 895	
25	ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac	2736
	Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp	
	900 905 910	
30	aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc	2784
	Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe	
	915 920 925	
35	agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca	2832
	Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr	
	930 935 940	
40	gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg	2880
	Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu	
	945 950 955 960	
45	tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac	2928
	Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn	
	965 970 975	
50	gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc	2976
	Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu	
	980 985 990	
55	tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg	3024
	Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu	
	995 1000 1005	
60	ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac	3072
	Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn	
	1010 1015 1020	
65	aga tcc gac acg gac gag gac aag acg tgc gtc cac ttc gag gag gac	3120
	Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp	
	1025 1030 1035 1040	
70	ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc	3168
	Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser	
	1045 1050 1055	
75	ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc	3216
	Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro	
	1060 1065 1070	
80	ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga	3264
	Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg	
	1075 1080 1085	

	gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg 3312															
	Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val				1090 1095 1100											
5	gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg 3360															
	Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg				1105 1110 1115 1120											
10	cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg 3408															
	Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp				1125 1130 1135											
15	agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa 3456															
	Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln				1140 1145 1150											
20	gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag 3504															
	Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu				1155 1160 1165											
25	ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc 3552															
	Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser				1170 1175 1180											
30	ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg 3600															
	Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg				1185 1190 1195 1200											
35	ccc ctg ccg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg 3648															
	Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly				1205 1210 1215											
40	cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac 3696															
	Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His				1220 1225 1230											
45	cgt gag gat gca gcc gag ctt gac gac gac tgc gag gac agc tgc tgc 3744															
	Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys				1235 1240 1245											
50	ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag ccg tgc ccg 3792															
	Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg				1250 1255 1260											
55	agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac 3840															
	Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn				1265 1270 1275 1280											
60	cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat 3888															
	Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp				1295 1290 1295											
65	cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg 3936															
	His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu				1300 1305 1310											
70	gag agg cct gac att gat ccc ggc agc acc gag ccg gtc ttc ctc agc 3984															
	Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser				1315 1320 1325											
75	gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg 4032															
	Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val				1330 1335 1340											



	aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag	4080
	Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln	
	1345 1350 1355 1360	
5	agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg	4128
	Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val	
	1365 1370 1375	
10	gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt	4176
	Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly	
	1380 1385 1390	
15	gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc	4224
	Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val	
	1395 1400 1405	
20	atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca	4272
	Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser	
	1410 1415 1420	
25	tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc	4320
	Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe	
	1425 1430 1435 1440	
30	atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac	4368
	Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr	
	1445 1450 1455	
35	tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc	4416
	Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys	
	1460 1465 1470	
40	cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac	4464
	Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn	
	1475 1480 1485	
45	ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga	4512
	Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly	
	1490 1495 1500	
50	tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag	4560
	Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln	
	1505 1510 1515 1520	
55	cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc	4608
	Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser	
	1525 1530 1535	
60	ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc	4656
	Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val	
	1540 1545 1550	
65	gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag	4704
	Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu	
	1555 1560 1565	
70	gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc	4752
	Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg	
	1570 1575 1580	
75	agg aag gcc cag cgc cgg ccc tac tat gcc gac tac tcg ccc acg cgc	4800
	Arg Lys Ala Gln Arg Arg Pro Tyr Tyr Ala Asp Tyr Ser Pro Thr Arg	
	1585 1590 1595 1600	

	cgc tgg att cac tcg ctg tgc acc agc cac tat ctc gac ctc ttc atc	4848
	Arg Trp Ile His Ser Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile	
	1605 1610 1615	
5	acc ttc atc atc tgt gtc aac gtc atc acc atg tcc atg gag cac tat	4896
	Thr Phe Ile Ile Cys Val Asn Val Ile Thr Met Ser Met Glu His Tyr	
	1620 1625 1630	
10	aac caa ccc aag tcg ctg gac gag gcc ctc aag tac tgc aac tac gtc	4944
	Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu Lys Tyr Cys Asn Tyr Val	
	1635 1640 1645	
15	ttc acc atc gtg ttt gtc ttc gag gct gca ctg aag ctg gta gca ttt	4992
	Phe Thr Ile Val Phe Val Phe Glu Ala Ala Leu Lys Leu Val Ala Phe	
	1650 1655 1660	
20	ggg ttc cgt cgg ttc ttc aag gac agg tgg aac cag ctg gac ctg gcc	5040
	Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp Asn Gln Leu Asp Leu Ala	
	1665 1670 1675 1680	
	atc gtg ctg ctg tca ctc atg ggc atc acg ctg gag gag ata gag atg	5088
	Ile Val Leu Leu Ser Leu Met Gly Ile Thr Leu Glu Glu Ile Glu Met	
	1685 1690 1695	
25	agc gcc gcg ctg ccc atc aac ccc acc atc atc cgc atc atg cgc gtg	5136
	Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val	
	1700 1705 1710	
30	ctt cgc att gcc cgt gtg ctg aag ctg ctg aag atg gct acg ggc atg	5184
	Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr Gly Met	
	1715 1720 1725	
35	cgc gcc ctg ctg gac act gtg gtg caa gct ctc ccc cag gtg ggg aac	5232
	Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val Gly Asn	
	1730 1735 1740	
40	ctg ggc ctt ctt ttc atg ctc ctg ttt ttt atc tat gct gcg ctg gga	5280
	Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly	
	1745 1750 1755 1760	
	gtg gag ctg ttc ggg agg ctg gag tgc agt gaa gac aac ccc tgc gag	5328
	Val Glu Leu Phe Gly Arg Leu Glu Cys Ser Glu Asp Asn Pro Cys Glu	
	1765 1770 1775	
45	ggc ctg agc agg cac gcc acc ttc agc aac ttc ggc atg gcc ttc ctc	5376
	Gly Leu Ser Arg His Ala Thr Phe Ser Asn Phe Gly Met Ala Phe Leu	
	1780 1785 1790	
50	acg ctg ttc cgc gtg tcc acg ggg gac aac tgg aac ggg atc atg aag	5424
	Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys	
	1795 1800 1805	
55	gac acg ctg cgc gag tgc tcc cgt gag gac aag cac tgc ctg agc tac	5472
	Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp Lys His Cys Leu Ser Tyr	
	1810 1815 1820	
60	ctg ccg gcc ccg tcg ccc gtc tac ttc gtg acc ttc gtg ctg gtg ccc	5520
	Leu Pro Ala Pro Ser Pro Val Tyr Phe Val Thr Phe Val Leu Val Pro	
	1825 1830 1835 1840	
	cag ttc gtg ctg gtg aac gtg gtg gtg gcc gtg ctc atg aag cac ctg	5568
	Gln Phe Val Leu Val Asn Val Val Val Ala Val Leu Met Lys His Leu	
	1845 1850 1855	

	gag gag agc aac aag gag gct cgg gag gat gcg gag ctg gac gcc gag	5616
	Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp Ala Glu Leu Asp Ala Glu	
	1860 1865 1870	
5	atc gag ctg gag atg gcg cag gcc ccc ggg agt gca cgc cgg gtg gac	5664
	Ile Glu Leu Glu Met Ala Gln Gly Pro Gly Ser Ala Arg Arg Val Asp	
	1875 1880 1885	
10	gcg gac agg cct ccc ttg ccc cag gag agt ccg gcc gcc agg gac gcc	5712
	Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser Pro Gly Ala Arg Asp Ala	
	1890 1895 1900	
15	cca aac ctg gtt gca cgc aag gtg tcc gtg tcc agg atg ctc tcg ctg	5760
	Pro Asn Leu Val Ala Arg Lys Val Ser Val Ser Arg Met Leu Ser Leu	
	1905 1910 1915 1920	
20	ccc aac gac agc tac atg ttc agg ccc gtg gtg cct gcc tcg gcg ccc	5808
	Pro Asn Asp Ser Tyr Met Phe Arg Pro Val Val Pro Ala Ser Ala Pro	
	1925 1930 1935	
25	cac ccc cgc ccg ctg cag gag gtg gag atg gag acc tat ggg gcc gcc	5856
	His Pro Arg Pro Leu Gln Glu Val Glu Met Glu Thr Tyr Gly Ala Gly	
	1940 1945 1950	
30	acc ccc ttg ggc tcc gtt gcc tct gtg cac tct ccg ccc gca gag tcc	5904
	Thr Pro Leu Gly Ser Val Ala Ser Val His Ser Pro Pro Ala Glu Ser	
	1955 1960 1965	
35	tgt gcc tcc ctc cag atc cca ctg gct gtg tcg tcc cca gcc agg agc	5952
	Cys Ala Ser Leu Gln Ile Pro Leu Ala Val Ser Ser Pro Ala Arg Ser	
	1970 1975 1980	
40	ggc gag ccc ctc cac gcc ctg tcc cct cgg gcc aca gcc cgc tcc ccc	6000
	Gly Glu Pro Leu His Ala Leu Ser Pro Arg Gly Thr Ala Arg Ser Pro	
	1985 1990 1995 2000	
45	agt ctc agc cgg ctg ctc tgc aga cag gag gct gtg cac acc gat tcc	6048
	Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu Ala Val His Thr Asp Ser	
	2005 2010 2015	
50	ttg aag gga aga ttg aca gcc cta ggg aca ccc tgg atc ctg cag agc	6096
	Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr Pro Trp Ile Leu Gln Ser	
	2020 2025 2030	
55	ctg gtg aga aaa ccc cgg	6114
	Leu Val Arg Lys Pro Arg	
	2035	
60	<210> 11	
	<211> 5469	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> CDS	
	<222> (1)..(5469)	
	<400> 11	
	atg gct gag agc gcc tcc ccg ccc tcc tca tct gca gca gcc cca gcc	48
	Met Ala Glu Ser Ala Ser Pro Pro Ser Ser Ser Ala Ala Ala Pro Ala	
	1 5 10 15	

	gct gag cca gga gtc acc acg gag cag ccc gga ccc cgg agc ccc cca	96
	Ala Glu Pro Gly Val Thr Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro	
	20 25 30	
5	tcc tcc ccg cca ggc ctg gag gag cct ctg gat gga gct gat cct cat	144
	Ser Ser Pro Pro Gly Leu Glu Glu Pro Leu Asp Gly Ala Asp Pro His	
	35 40 45	
10	gtc cca cac cca gac ctg gcg cct att gcc ttc ttc tgc ctg cga cag	192
	Val Pro His Pro Asp Leu Ala Pro Ile Ala Phe Phe Cys Leu Arg Gln	
	50 55 60	
15	acc acc agc ccc cgg aac tgg tgc atc aag atg gtg tgc aac ccg tgg	240
	Thr Thr Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp	
	65 70 75 80	
20	ttt gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt	288
	Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu	
	85 90 95	
25	ggc atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc	336
	Gly Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys	
	100 105 110	
30	aag atc atg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg	384
	Lys Ile Met Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met	
	115 120 125	
35	gag atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc	432
	Glu Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys	
	130 135 140	
40	tac ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca	480
	Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala	
	145 150 155 160	
45	ggg atg gtc gag tac tcc ctg gac ctt cag aac atc aac ctg tca gcc	528
	Gly Met Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala	
	165 170 175	
50	atc cgc acc gtg cgc gtc ctg agg ccc ctc aaa gcc atc aac cgc gtg	576
	Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val	
	180 185 190	
55	ccc agt atg cgg atc ctg gtg aac ctg ctc ctg gac aca ctg ccc atg	624
	Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met	
	195 200 205	
60	ctg.ggg aat gtc ctg ctg ctc tgc ttc ttt gtc ttc ttc atc ttt ggc	672
	Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly	
	210 215 220	
65	atc ata ggt gtg cag ctc tgg gcg ggc ctg ctg cgt aac cgc tgc ttc	720
	Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe	
	225 230 235 240	
70	ctg gag gag aac ttc acc ata caa ggg gat gtg gcc ttg ccc cca tac	768
	Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr	
	245 250 255	
75	tac cag ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg tcg	816
	Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser	
	260 265 270	

	ggc gac aat ggg ata atg ggc tgc cat gag atc ccc ccg ctc aag gag	864
	Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu	
	275 280 285	
5	cag ggc cgt gag tgc tgc ctg tcc aag gac gac gtc tac gac ttt ggg	912
	Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly	
	290 295 300	
10	ggc ggg cgc cag gac ctc aat gcc agc ggc ctc tgt gtc aac tgg aac	960
	Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn	
	305 310 315 320	
15	cgt tac tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt	1008
	Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly	
	325 330 335	
20	gcc atc aac ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag	1056
	Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln	
	340 345 350	
	gtg atc act ctg gaa ggc tgg gtg gag atc atg tac tac gtg atg gat	1104
	Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp	
	355 360 365	
25	gct cac tcc ttc tac aac ttc atc tac ttc atc ctg ctt atc ata gtg	1152
	Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val	
	370 375 380	
30	ggc tcc ttc ttc atg atc aac ctg tgc ctc gtt gtc ata gcg acc cag	1200
	Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln	
	385 390 395 400	
35	ttc tcg gag acc aag caa cgg gag cac cgg ctg atg ctg gag cag cgg	1248
	Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg	
	405 410 415	
40	cag cgc tac ctg tcc tcc agc acg gtg gcc agc tac gcc gag cct ggc	1296
	Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly	
	420 425 430	
	gac tgc tac gag gag atc ttc cag tat gtc tgc cac atc ctg cgc aag	1344
	Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys	
	435 440 445	
45	gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg cag agc cgg cgc	1392
	Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg	
	450 455 460	
50	cag gcc ctg ggc ccg gag gcc ccg gcc ccc gcc aaa cct ggg ccc cac	1440
	Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His	
	465 470 475 480	
55	gcc aag gag ccc cgg cac tac cag ctg tgc ccg caa cat agc ccc ctg	1488
	Ala Lys Glu Pro Arg His Tyr Gln Leu Cys Pro Gln His Ser Pro Leu	
	485 490 495	
60	gat gcg acg ccc cac acc ctg gtg cag ccc atc ccc gcc acg ctg gat	1536
	Asp Ala Thr Pro His Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala	
	500 505 510	
	tcc gat ccc gcc agc tgc cct tgc tgc cag cat gag gac ggc cgg cgg	1584
	Ser Asp Pro Ala Ser Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg	
	515 520 525	

	ccc	tcg	ggc	ctg	ggc	agc	acc	gac	tcg	ggc	cag	gag	ggc	tcg	ggc	tcg	1632
	Pro	Ser	Gly	Leu	Gly	Ser	Thr	Asp	Ser	Gly	Gln	Glu	Gly	Ser	Gly	Ser	
	530						535					540					
5	ggg	agc	tcg	gct	ggc	ggc	gag	gac	gag	gcg	gat	ggg	gac	ggg	gcc	cgg	1680
	Gly	Ser	Ser	Ala	Gly	Gly	Glu	Asp	Glu	Ala	Asp	Gly	Asp	Gly	Ala	Arg	
	545					550					555					560	
10	agc	agc	gag	gac	gga	gcc	tcg	tca	gaa	ctg	ggg	aag	gag	gag	gag	gag	1728
	Ser	Ser	Glu	Asp	Gly	Ala	Ser	Ser	Glu	Leu	Gly	Lys	Glu	Glu	Glu	Glu	
					565					570					575		
15	gag	gag	cag	gcg	gat	ggg	gcg	gtc	tcg	ctg	tgc	ggg	gat	gtg	tgg	cgg	1776
	Glu	Glu	Gln	Ala	Asp	Gly	Ala	Val	Trp	Leu	Cys	Gly	Asp	Val	Trp	Arg	
				580					585					590			
20	gag	acg	cga	gcc	aag	ctg	cgc	ggc	atc	gtg	gac	agc	aag	tac	ttc	aac	1824
	Glu	Thr	Arg	Ala	Lys	Leu	Arg	Gly	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Asn	
			595					600					605				
25	cgg	ggc	atc	atg	atg	gcc	atc	ctg	gtc	aac	acc	gtc	agc	atg	ggc	atc	1872
	Arg	Gly	Ile	Met	Met	Ala	Ile	Leu	Val	Asn	Thr	Val	Ser	Met	Gly	Ile	
	610						615					620					
30	gag	cac	cac	gag	cag	ccg	gag	gag	ctg	acc	aac	atc	ctg	gag	atc	tgc	1920
	Glu	His	His	Glu	Gln	Pro	Glu	Glu	Leu	Thr	Asn	Ile	Leu	Glu	Ile	Cys	
	625					630					635					640	
35	aat	gtg	gtc	ttc	acc	agc	atg	ttt	gcc	ctg	gag	atg	atc	ctg	aag	ctg	1968
	Asn	Val	Val	Phe	Thr	Ser	Met	Phe	Ala	Leu	Glu	Met	Ile	Leu	Lys	Leu	
					645					650					655		
40	gct	gca	ttt	ggg	ctc	ttc	gac	tac	ctg	cgt	aac	ccc	tac	aac	atc	ttc	2016
	Ala	Ala	Phe	Gly	Leu	Phe	Asp	Tyr	Leu	Arg	Asn	Pro	Tyr	Asn	Ile	Phe	
				660					665					670			
45	gac	agc	atc	att	gtc	atc	atc	agc	atc	tgg	gag	atc	gtg	ggg	cag	gcg	2064
	Asp	Ser	Ile	Ile	Val	Ile	Ile	Ser	Ile	Trp	Glu	Ile	Val	Gly	Gln	Ala	
			675					680					685				
50	gac	ggc	ggg	ctg	tcg	gtg	ctg	cgg	acc	ttc	cgg	ctg	ctg	cgc	gtg	ctg	2112
	Asp	Gly	Gly	Leu	Ser	Val	Leu	Arg	Thr	Phe	Arg	Leu	Leu	Arg	Val	Leu	
	690						695					700					
55	aaa	ctg	gtg	cgc	ttc	atg	cct	gcc	ctg	cgg	cgc	cag	ctc	gtg	gtg	ctc	2160
	Lys	Leu	Val	Arg	Phe	Met	Pro	Ala	Leu	Arg	Arg	Gln	Leu	Val	Val	Leu	
	705					710					715					720	
60	atg	aag	acc	atg	gac	aac	gtg	gcc	acc	ttc	tgc	atg	ctg	ctc	atg	ctc	2208
	Met	Lys	Thr	Met	Asp	Asn	Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	
					725					730					735		
65	ttc	atc	ttc	atc	ttc	agc	atc	ctt	ggg	atg	cat	att	ttt	ggc	tgc	aag	2256
	Phe	Ile	Phe	Ile	Phe	Ser	Ile	Leu	Gly	Met	His	Ile	Phe	Gly	Cys	Lys	
				740					745					750			
70	ttc	agc	ctc	cgc	acg	gac	act	gga	gac	acg	gtg	ccc	gac	agg	aag	aac	2304
	Phe	Ser	Leu	Arg	Thr	Asp	Thr	Gly	Asp	Thr	Val	Pro	Asp	Arg	Lys	Asn	
				755				760					765				
75	ttc	gac	tcg	ctg	ctg	tgg	gcc	atc	gtc	act	gtg	ttc	cag	atc	ctc	acc	2352
	Phe	Asp	Ser	Leu	Leu	Trp	Ala	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	
	770						775						780				

	cag	gag	gac	tgg	aac	gtc	gtt	ctc	tac	aat	ggc	atg	gcc	tcc	act	tct	2400
	Gln	Glu	Asp	Trp	Asn	Val	Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	900
	785					790					795						
5	ccc	tgg	gcc	tcc	ctc	tac	ttt	gtc	gcc	ctc	atg	acc	ttc	ggc	aac	tat	2448
	Pro	Trp	Ala	Ser	Leu	Tyr	Phe	Val	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	815
					805					810					815		
10	gtg	ctc	ttc	aac	ctg	ctg	gtg	gcc	atc	ctg	gtg	gag	ggc	ttc	cag	gcg	2496
	Val	Leu	Phe	Asn	Leu	Leu	Val	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	820
				820					225					830			
15	gag	ggt	gac	gcc	aat	cgc	tcc	tac	tgc	gac	gag	gac	cag	agc	tca	tcc	2544
	Glu	Gly	Asp	Ala	Asn	Arg	Ser	Tyr	Ser	Asp	Glu	Asp	Gln	Ser	Ser	Ser	835
			835					840					845				
20	aac	ata	gaa	gag	ttt	gat	aag	ctc	cag	gaa	ggc	ctg	gac	agc	agc	gga	2592
	Asn	Ile	Glu	Glu	Phe	Asp	Lys	Leu	Gln	Glu	Gly	Leu	Asp	Ser	Ser	Gly	850
		850					855					860					
25	gat	ccc	aag	ctc	tgc	cca	atc	ccc	atg	acc	ccc	aat	ggg	cac	ctg	gac	2640
	Asp	Pro	Lys	Leu	Cys	Pro	Ile	Pro	Met	Thr	Pro	Asn	Gly	His	Leu	Asp	865
						870					875					880	
30	ccc	agt	ctc	cca	ctg	ggt	ggg	cac	cta	ggt	cct	gct	ggg	gct	gcg	gga	2688
	Pro	Ser	Leu	Pro	Leu	Gly	Gly	His	Leu	Gly	Pro	Ala	Gly	Ala	Ala	Gly	885
					885					890					895		
35	cct	gcc	ccc	cga	ctc	tca	ctg	cag	ccg	gac	ccc	atg	ctg	gtg	gcc	ctg	2736
	Pro	Ala	Pro	Arg	Leu	Ser	Leu	Gln	Pro	Asp	Pro	Met	Leu	Val	Ala	Leu	900
				900					905					910			
40	ggc	tcc	cga	aag	agc	agc	gtc	atg	tct	cta	ggg	agg	atg	agc	tat	gac	2784
	Gly	Ser	Arg	Lys	Ser	Ser	Val	Met	Ser	Leu	Gly	Arg	Met	Ser	Tyr	Asp	915
			915					920					925				
45	cag	cgc	tcc	ctg	tcc	agc	tcc	cgg	agc	tcc	tac	tac	ggg	cca	tgg	ggc	2832
	Gln	Arg	Ser	Leu	Ser	Ser	Ser	Arg	Ser	Ser	Tyr	Tyr	Gly	Pro	Trp	Gly	930
		930					935					940					
50	cgc	agc	gcg	gcc	tgg	gcc	agc	cgt	cgc	tcc	agc	tgg	aac	agc	ctc	aag	2880
	Arg	Ser	Ala	Ala	Trp	Ala	Ser	Arg	Arg	Ser	Ser	Trp	Asn	Ser	Leu	Lys	945
						950					955					960	
55	cac	aag	ccg	ccg	tgc	gcg	gag	cat	gag	tcc	ctg	ctc	tct	gcg	gag	cgc	2928
	His	Lys	Pro	Pro	Ser	Ala	Glu	His	Glu	Ser	Leu	Leu	Ser	Ala	Glu	Arg	965
					965				970					975			
60	ggc	ggc	ggc	gcc	cgg	gtc	tgc	gag	gtt	gcc	gcg	gac	gag	ggg	ccg	ccg	2976
	Gly	Gly	Gly	Ala	Arg	Val	Cys	Glu	Val	Ala	Ala	Asp	Glu	Gly	Pro	Pro	980
				980					985					990			
65	cgg	gcc	gca	ccc	ctg	cac	acc	cca	cac	gcc	cac	cac	gtt	cat	cac	ggc	3024
	Arg	Ala	Ala	Pro	Leu	His	Thr	Pro	His	Ala	His	His	Val	His	His	Gly	995
			995				1000						1005				
70	ccc	cat	ctg	gcg	cac	cgc	cac	cgc	cac	cac	cgc	cgg	acg	ctg	tcc	ctc	3072
	Pro	His	Leu	Ala	His	Arg	His	Arg	His	His	Arg	Arg	Thr	Leu	Ser	Leu	1010
		1010					1015					1020					
75	gac	aac	agg	gac	tgc	gtg	gac	ctg	gcc	gag	ctg	gtg	ccc	gcg	gtg	ggc	3120
	Asp	Asn	Arg	Asp	Ser	Val	Asp	Leu	Ala	Glu	Leu	Val	Pro	Ala	Val	Gly	1025
					1030					1035					1040		

	gac cac ccc cgg gac gcc tgg agg gcg gca ggc ccg gcc ccc ggg cat	3168
	Ala His Pro Arg Ala Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His	
	1045 1050 1055	
5	gag gac tgc aat ggc agg atg ccc agc atc gcc aaa gac gtc ttc acc	3216
	Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr	
	1060 1065 1070	
10	aag atg ggc gac cgc ggg gat cgc ggg gag gat gag gag gaa atc gac	3264
	Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp Glu Glu Ile Asp	
	1075 1080 1085	
15	tac acc ctg tgc ttc cgc gtc cgc aag atg atc gac gtc tat aag ccc	3312
	Tyr Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro	
	1090 1095 1100	
20	gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc	3360
	Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro	
	1105 1110 1115 1120	
	gag aac agg ttc cgg gtc ctg tgt cag acc atc att gcc cac aaa ctc	3408
	Glu Asn Arg Phe Arg Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu	
	1125 1130 1135	
25	ttc gac tac gtc gtc ctg gcc ttc atc ttt ctc aac tgc atc acc atc	3456
	Phe Asp Tyr Val Val Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile	
	1140 1145 1150	
30	gcc ctg gag cgg cct cag atc gag gcc ggc agc acc gaa cgc atc ttt	3504
	Ala Leu Glu Arg Pro Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe	
	1155 1160 1165	
35	ctc acc gtg tcc aac tac atc ttc acg gcc atc ttc gtg ggc gag atg	3552
	Leu Thr Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met	
	1170 1175 1180	
40	aca ttg aag gta gtc tcg ctg ggc ctg tac ttc ggc gag cag gcg tac	3600
	Thr Leu Lys Val Val Ser Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr	
	1185 1190 1195 1200	
	cta cgc agc agc tgg aac gtg ctg gat ggc ttt ctt gtc ttc gtg tcc	3648
	Leu Arg Ser Ser Trp Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser	
	1205 1210 1215	
45	atc atc gac atc gtg gtg tcc ctg gcc tca gcc ggc gga gcc aag atc	3696
	Ile Ile Asp Ile Val Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile	
	1220 1225 1230	
50	ttg ggg gtc ctc cga gtc ttg cgg ctc ctg cgc acc cta cgc ccc ctg	3744
	Leu Gly Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu	
	1235 1240 1245	
55	cgt gtc atc agc cgg gcg ccg ggc ctg aag ctg gtg gtg gag aca ctc	3792
	Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu	
	1250 1255 1260	
60	atc tcc tcc ctc aag ccc atc ggc aac atc gtg ctc atc tgc tgt gcc	3840
	Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala	
	1265 1270 1275 1280	
	ttc ttc atc atc ttt ggc atc ctg gga gtg cag ctc ttc aag ggc aag	3888
	Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys	
	1285 1290 1295	



	ttc tac cac tgt ctg ggc gtg gac acc cgc aac atc acc aac cgc tgc	3936
	Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile Thr Asn Arg Ser	
	1300 1305 1310	
5	gac tgc atg gcc gcc aac tac cgc tgg gtc cat cac aaa tac aac ttc	3984
	Asp Cys Met Ala Ala Asn Tyr Arg Trp Val His His Lys Tyr Asn Phe	
	1315 1320 1325	
10	gac aac ctg ggc cag gct ctg atg tcc ctc ttt gtc ctg gca tcc aag	4032
	Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ala Ser Lys	
	1330 1335 1340	
15	gat ggt tgg gtg aac atc atg tac aat gga ctg gat gct gtc gct gtg	4080
	Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp Ala Val Ala Val	
	1345 1350 1355 1360	
20	gac cag cag cct gtg acc aac cac aac ccc tgg atg ctg ctg tac ttc	4128
	Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met Leu Leu Tyr Phe	
	1365 1370 1375	
	atc tcc ttc ctg ctc atc gtc agc ttc ttt gtg ctc aac atg ttt gtg	4176
	Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val	
	1380 1385 1390	
25	ggt gtc gtg gtg gag aac ttc cac aag tgc cgg cag cac cag gag gct	4224
	Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln His Gln Glu Ala	
	1395 1400 1405	
30	gaa gag gca cgg cgg cgt gag gag aag cgg ctg cgg cgc ctg gag aag	4272
	Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys	
	1410 1415 1420	
35	aag cgc cgg aag gcc cag cgg ctg ccc tac tat gcc acc tat tgt cac	4320
	Lys Arg Arg Lys Ala Gln Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys His	
	1425 1430 1435 1440	
40	acc cgg ctg ctc atc cac tcc atg tgc acc agc cac tac ctg gac atc	4368
	Thr Arg Leu Leu Ile His Ser Met Cys Thr Ser His Tyr Leu Asp Ile	
	1445 1450 1455	
	ttc atc acc ttc atc atc tgc ctc aac gtg gtc acc atg tcc ctg gag	4416
	Phe Ile Thr Phe Ile Ile Cys Leu Asn Val Val Thr Met Ser Leu Glu	
	1460 1465 1470	
45	cac tac aat cag ccc acg tcc ctg gag aca gcc ctc aag tac tgc aac	4464
	His Tyr Asn Gln Pro Thr Ser Leu Glu Thr Ala Leu Lys Tyr Cys Asn	
	1475 1480 1485	
50	tat atg ttc acc act gtc ttt gtg ctg gag gct gtg ctg aag ctg gtg	4512
	Tyr Met Phe Thr Thr Val Phe Val Leu Glu Ala Val Leu Lys Leu Val	
	1490 1495 1500	
55	gca ttt ggt ctg agg cgc tta ttc aag gac cga tgg aac cag ctg gac	4560
	Ala Phe Gly Leu Arg Arg Leu Phe Lys Asp Arg Trp Asn Gln Leu Asp	
	1505 1510 1515 1520	
60	ctg gcc att gtg cta ctg tca gtc atg ggc atc acc ctg gag gag atc	4608
	Leu Ala Ile Val Leu Leu Ser Val Met Gly Ile Thr Leu Glu Glu Ile	
	1525 1530 1535	
	gag atc aat gcg gcc ctg ccc atc aat ccc acc atc atc cgc atc atg	4656
	Glu Ile Asn Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met	
	1540 1545 1550	

	agg gtt ctg cgc att gcc cga gtg ctg aag ctg ttg aag atg gcc aca	4704
	Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr	
	1555 1560 1565	
5	gga atg cgg gcc ctg ctg gac acg gtg gtg caa gct ttg ccc cag gtg	4752
	Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val	
	1570 1575 1580	
10	ggc aac ctg ggc ctc ctc ttc atg ctg ctc ttc ttc atc tat gct gct	4800
	Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala	
	1585 1590 1595 1600	
15	ctc ggg gtg gag ctc ttt ggg aag ctg gtc tgc aac gac gag aac ccg	4848
	Leu Gly Val Glu Leu Phe Gly Lys Leu Val Cys Asn Asp Glu Asn Pro	
	1605 1610 1615	
20	tgc gag ggc atg agc cgg cat gcc acc ttc gag aac ttc ggc atg gcc	4896
	Cys Glu Gly Met Ser Arg His Ala Thr Phe Glu Asn Phe Gly Met Ala	
	1620 1625 1630	
25	ttc ctc aca ctc ttc cag gtc tcc acg ggt gac aac tgg aac ggg atc	4944
	Phe Leu Thr Leu Phe Gln Val Ser Thr Gly Asp Asn Trp Asn Gly Ile	
	1635 1640 1645	
30	atg aag gac acg ctg cgg gac tgc acc cac gac gag cgc agc tgc ctg	4992
	Met Lys Asp Thr Leu Arg Asp Cys Thr His Asp Glu Arg Ser Cys Leu	
	1650 1655 1660	
35	agc agc ctg cag ttt gtg tgc ccg ctg tac ttc gtg agc ttc gtg ctc	5040
	Ser Ser Leu Gln Phe Val Ser Pro Leu Tyr Phe Val Ser Phe Val Leu	
	1665 1670 1675 1680	
40	acc gcg cag ttc gtg ctc atc aac gtg gtg gtg gct gtg ctc atg aag	5088
	Thr Ala Gln Phe Val Leu Ile Asn Val Val Val Ala Val Leu Met Lys	
	1685 1690 1695	
45	cac ctg gac gac agc aac aag gag gcg cag gag gac gcc gag atg gat	5136
	His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp Ala Glu Met Asp	
	1700 1705 1710	
50	gcc gag ctc gag ctg gag atg gcc cat ggc ctg ggc cct ggc ccg agg	5184
	Ala Glu Leu Glu Leu Glu Met Ala His Gly Leu Gly Pro Gly Pro Arg	
	1715 1720 1725	
55	ctg cct acc ggc tcc ccg ggc gcc cct ggc cga ggg ccg gga ggg gcg	5232
	Leu Pro Thr Gly Ser Pro Gly Ala Pro Gly Arg Gly Pro Gly Gly Ala	
	1730 1735 1740	
60	ggc ggc ggg ggc gac acc gat ggc ggc ttg tgc cgg cgc tgc tac tgc	5280
	Gly Gly Gly Gly Asp Thr Asp Gly Gly Leu Cys Arg Arg Cys Tyr Ser	
	1745 1750 1755 1760	
65	cct gcc cag gag aac ctg tgg ctg gac agc gtc tct tta atc atc aag	5328
	Pro Ala Gln Glu Asn Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys	
	1765 1770 1775	
70	gac tcc ttg gag ggg gag ctg acc atc atc gac aac ctg tgc ggc tcc	5376
	Asp Ser Leu Glu Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser	
	1780 1785 1790	
75	atc ttc cac cac tac tcc tgc cct gcc ggc tgc aag aag tgt cac cac	5424
	Ile Phe His His Tyr Ser Ser Pro Ala Gly Cys Lys Lys Cys His His	
	1795 1800 1805	

gac aag caa gag aca ggt cct cgt cca tcc tgc tgg gtg acg acc 5469  
 Asp Lys Gln Glu Thr Gly Pro Arg Pro Ser Cys Trp Val Thr Thr  
 1810 1815 1820

5  
 <210> 12  
 <211> 5505  
 <212> DNA  
 <213> Rattus sp.

10  
 <220>  
 <221> CDS  
 <222> (1)..(5505)

15  
 <400> 12  
 atg gct gac agc aac tta ccg ccc tca tct gca gca gcc ccg gcc cct 48  
 Met Ala Asp Ser Asn Leu Pro Pro Ser Ser Ala Ala Ala Pro Ala Pro  
 1 5 10 15

20  
 gag ccg gga atc act gag cag ccg ggg ccc ccg agt ccc cct cca tcc 96  
 Glu Pro Gly Ile Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro Pro Ser  
 20 25 30

25  
 cct cca ggc ctg gag gag cca ttg gaa gga acc aac cct gac gtc cca 144  
 Pro Pro Gly Leu Glu Glu Pro Leu Glu Gly Thr Asn Pro Asp Val Pro  
 35 40 45

30  
 cat cca gac ctg gct cct gtt gct ttc ttc tgc ctg cgc cag acc acg 192  
 His Pro Asp Leu Ala Pro Val Ala Phe Phe Cys Leu Arg Gln Thr Thr  
 50 55 60

35  
 agc cca ccg aac tgg tgc atc aag atg gtt tgt aac ccg tgg ttc gag 240  
 Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp Phe Glu  
 65 70 75 80

40  
 tgt gtg agc atg ctg gtt att ctg ctg aac tgt gtg acc ctg ggc atg 288  
 Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met  
 85 90 95

45  
 tac cag cca tgt gat gac atg gag tgc ctg tgc gac cgt tgc aag atc 336  
 Tyr Gln Pro Cys Asp Asp Met Glu Cys Leu Ser Asp Arg Cys Lys Ile  
 100 105 110

50  
 ctg cag gtc ttc gat gac ttc atc ttc atc ttc ttt gcc atg gag atg 384  
 Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met  
 115 120 125

55  
 gtg ctt aag atg gtg gcc ctg ggc att ttt ggc aag aag tgc tac ctc 432  
 Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu  
 130 135 140

60  
 gga gac aca tgg aac ccg ctg gat ttc ttc att gtc atg gca ggg atg 480  
 Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Met  
 145 150 155 160

65  
 gtt gag tac tct ctg gac cta cag aac atc aac ctg tca gcc atc cgc 528  
 Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala Ile Arg  
 165 170 175

70  
 act gtg cgt gtc ctg agg cct ctc aaa gcc atc aac cgt gta ccc agc 576  
 Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val Pro Ser  
 180 185 190

atg ccg atc ctg gtg aac ctg ctg ctc gac acg ctg ccc atg ctg ggg 624

	Met	Arg	Ile	Leu	Val	Asn	Leu	Leu	Leu	Asp	Thr	Leu	Pro	Met	Leu	Gly	
			195					200					205				
5	aac	gtg	ctc	ctg	ctc	tgt	ttc	ttc	gtc	ttc	ttc	atc	ttc	ggc	atc	att	672
	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	Phe	Gly	Ile	Ile	
		210					215					220					
10	ggc	gtg	cag	ctc	tgg	gca	ggc	ctg	cta	cgg	aac	cgc	tgc	ttc	ctg	gaa	720
	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg	Cys	Phe	Leu	Glu	
		225				230					235					240	
15	gag	aac	ttc	acc	ata	caa	ggg	gat	gtg	gcc	ctg	ccc	cct	tat	tac	caa	768
	Glu	Asn	Phe	Thr	Ile	Gln	Gly	Asp	Val	Ala	Leu	Pro	Pro	Tyr	Tyr	Gln	
					245					250					255		
20	cca	gag	gag	gat	gac	gag	atg	ccc	ttt	atc	tgc	tcc	ctg	act	ggg	gac	816
	Pro	Glu	Glu	Asp	Asp	Glu	Met	Pro	Phe	Ile	Cys	Ser	Leu	Thr	Gly	Asp	
				260					265					270			
25	aat	ggc	atc	atg	ggc	tgc	cac	gag	atc	ccc	cca	ctg	aag	gag	cag	ggc	864
	Asn	Gly	Ile	Met	Gly	Cys	His	Glu	Ile	Pro	Pro	Leu	Lys	Glu	Gln	Gly	
			275					280					285				
30	cgg	gaa	tgc	tgc	ctg	tcc	aaa	gat	gat	gtg	tat	gac	ttc	ggg	gcg	ggg	912
	Arg	Glu	Cys	Cys	Leu	Ser	Lys	Asp	Asp	Val	Tyr	Asp	Phe	Gly	Ala	Gly	
		290					295					300					
35	cgc	cag	gac	ctc	aac	gcc	agc	ggt	ctg	tgc	gtc	aac	tgg	aac	cgc	tac	960
	Arg	Gln	Asp	Leu	Asn	Ala	Ser	Gly	Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	
		305				310					315					320	
40	tac	aac	gtc	tgc	cgc	acg	ggc	aac	gcc	aac	cct	cac	aag	ggc	gcc	atc	1008
	Tyr	Asn	Val	Cys	Arg	Thr	Gly	Asn	Ala	Asn	Pro	His	Lys	Gly	Ala	Ile	
					325					330					335		
45	aac	ttt	gac	aac	att	ggc	tat	gcc	ggg	att	gtg	att	ttc	cag	gtg	atc	1056
	Asn	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Gly	Ile	Val	Ile	Phe	Gln	Val	Ile	
				340					345					350			
50	act	ctg	gaa	ggc	tgg	gtg	gag	atc	atg	tac	tat	gtg	atg	gac	gca	cat	1104
	Thr	Leu	Glu	Gly	Trp	Val	Glu	Ile	Met	Tyr	Tyr	Val	Met	Asp	Ala	His	
			355				360						365				
55	tct	ttc	tac	aac	ttc	atc	tac	ttc	att	ctg	ctc	atc	ata	gtg	ggc	tcc	1152
	Ser	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	
		370				375						380					
60	ttc	ttc	atg	atc	aac	ttg	tgc	ctc	gtt	gtc	ata	gca	acc	cag	ttc	tct	1200
	Phe	Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	
						390					395					400	
65	gag	acc	aag	caa	cgg	gag	cac	cgg	ctg	atg	ctg	gag	caa	cgc	cag	cgc	1248
	Glu	Thr	Lys	Gln	Arg	Glu	His	Arg	Leu	Met	Leu	Glu	Gln	Arg	Gln	Arg	
					405				410						415		
70	tac	ctg	tcc	tcc	agc	acg	gtg	gcc	agt	tac	gct	gag	ccc	ggt	gat	tgc	1296
	Tyr	Leu	Ser	Ser	Ser	Thr	Val	Ala	Ser	Tyr	Ala	Glu	Pro	Gly	Asp	Cys	
				420					425					430			
75	tat	gag	gag	atc	ttc	caa	tat	gtc	tgt	cac	atc	ctt	cgc	aaa	gcc	aag	1344
	Tyr	Glu	Glu	Ile	Phe	Gln	Tyr	Val	Cys	His	Ile	Leu	Arg	Lys	Ala	Lys	
			435					440					445				
80	cgc	cgt	gcc	cta	ggc	ctc	tac	cag	gcc	ctg	cag	aac	cgg	cgc	cag	gcc	1392

	Arg	Arg	Ala	Leu	Gly	Leu	Tyr	Gln	Ala	Leu	Gln	Asn	Arg	Arg	Gln	Ala	
	450						455					460					
5	atg	ggc	ccg	ggg	aca	cca	gcc	cct	gcc	aag	cct	ggg	ccc	cat	gcc	aag	1440
	Met	Gly	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Lys	Pro	Gly	Pro	His	Ala	Lys	
	465					470					475					480	
10	gag	ccc	agc	cac	tgc	aag	ctg	tgc	cca	cga	cac	agc	ccc	ctg	gac	ccc	1489
	Glu	Pro	Ser	His	Cys	Lys	Leu	Cys	Pro	Arg	His	Ser	Pro	Leu	Asp	Pro	
					485					490					495		
15	act	ccc	cac	aca	ctg	gtg	cag	ccc	atc	tct	gcc	att	ctg	gcc	tct	gac	1536
	Thr	Pro	His	Thr	Leu	Val	Gln	Pro	Ile	Ser	Ala	Ile	Leu	Ala	Ser	Asp	
				500					505					510			
20	ccc	agc	agc	tgc	cct	cac	tgc	cag	cac	gag	gca	ggc	agg	cgg	ccc	tct	1584
	Pro	Ser	Ser	Cys	Pro	His	Cys	Gln	His	Glu	Ala	Gly	Arg	Arg	Pro	Ser	
				515				520					525				
25	ggc	ctg	ggc	agc	act	gac	tca	ggc	cag	gaa	ggc	tca	ggt	tct	ggt	ggc	1632
	Gly	Leu	Gly	Ser	Thr	Asp	Ser	Gly	Gln	Glu	Gly	Ser	Gly	Ser	Gly	Gly	
		530					535					540					
30	tct	gca	gag	gcc	gaa	gcc	aat	ggg	gat	gga	ctc	cag	agc	agt	gag	gat	1680
	Ser	Ala	Glu	Ala	Glu	Ala	Asn	Gly	Asp	Gly	Leu	Gln	Ser	Ser	Glu	Asp	
	545				550						555					560	
35	ggg	gtc	tcc	tcg	gac	ctg	ggg	aag	gag	gag	gaa	cag	gag	gac	ggg	gca	1728
	Gly	Val	Ser	Ser	Asp	Leu	Gly	Lys	Glu	Glu	Glu	Gln	Glu	Asp	Gly	Ala	
					565					570					575		
40	ggc	cga	ctg	tgt	ggg	gat	gtg	tgg	cgc	gag	aca	cga	aaa	aag	ctg	cgg	1776
	Ala	Arg	Leu	Cys	Gly	Asp	Val	Trp	Arg	Glu	Thr	Arg	Lys	Lys	Leu	Arg	
				580					585					590			
45	ggc	atc	gtg	gac	agc	aag	tac	ttc	aac	aga	ggt	atc	atg	atg	gct	atc	1824
	Gly	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Asn	Arg	Gly	Ile	Met	Met	Ala	Ile	
		595					600						605				
50	ctg	gtg	aac	aca	gtc	agc	atg	ggc	atc	gag	cac	cac	gaa	cag	ccc	gag	1872
	Leu	Val	Asn	Thr	Val	Ser	Met	Gly	Ile	Glu	His	His	Glu	Gln	Pro	Glu	
		610					615					620					
55	gag	ctg	acc	aac	atc	ctg	gag	atc	tgc	aat	gtg	gtc	ttc	acc	agt	atg	1920
	Glu	Leu	Thr	Asn	Ile	Leu	Glu	Ile	Cys	Asn	Val	Val	Phe	Thr	Ser	Met	
	625					630					635					640	
60	ttt	gcc	ctg	gag	atg	atc	ctg	aaa	ctg	gcc	gcc	ttt	ggg	ctc	ttc	gac	1968
	Phe	Ala	Leu	Glu	Met	Ile	Leu	Lys	Leu	Ala	Ala	Phe	Gly	Leu	Phe	Asp	
					645					650					655		
65	tac	ctg	cgg	aac	cct	tac	aac	atc	ttt	gac	agc	atc	atc	gtc	atc	atc	2016
	Tyr	Leu	Arg	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Ser	Ile	Ile	Val	Ile	Ile	
				660					665					670			
70	agc	atc	tgg	gaa	atc	gtg	ggg	cag	gcg	gac	ggt	ggc	ctg	tct	gtg	ctg	2064
	Ser	Ile	Trp	Glu	Ile	Val	Gly	Gln	Ala	Asp	Gly	Gly	Leu	Ser	Val	Leu	
			675					680					685				
75	cgc	acc	ttc	cgg	ttg	ctg	cgg	gtg	ctg	aag	ctg	gtg	cgc	ttc	atg	cgg	2112
	Arg	Thr	Phe	Arg	Leu	Leu	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	Met	Pro	
		690					695					700					
80	gcg	ctg	cgg	cgc	cag	ctc	gtg	gtg	ctc	atg	aag	acc	atg	gac	aac	gtg	2160

	Ala	Leu	Arg	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	Asn	Val	
	705					710					715					720	
5	gcc	acc	ttc	tgc	atg	cta	ctc	atg	ctg	ttc	atc	ttc	atc	ttc	agc	atc	2208
	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	Ser	Ile	
					725					730					735		
10	ctt	ggg	atg	cat	atc	ttt	ggc	tgc	aaa	ttc	agc	ctc	cgc	acg	gac	acg	2256
	Leu	Gly	Met	His	Ile	Phe	Gly	Cys	Lys	Phe	Ser	Leu	Arg	Thr	Asp	Thr	
				740					745					750			
15	gga	gac	acc	gtt	cct	gac	agg	aag	aac	ttc	gat	tcc	tta	ctg	tgg	gcc	2304
	Gly	Asp	Thr	Val	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp	Ala	
			755					760					765				
	atc	gtc	aca	gtg	ttc	cag	atc	ctc	act	cag	gag	gac	tgg	aac	gtt	gtc	2352
	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	Asp	Trp	Asn	Val	Val	
		770				775						780					
20	ctg	tac	aat	ggc	atg	gcc	tcc	acc	acc	ccc	tgg	gcc	tcc	ctc	tat	ttt	2400
	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Thr	Pro	Trp	Ala	Ser	Leu	Tyr	Phe	
	785					790					795					800	
25	gtt	gcc	ctc	atg	acc	ttt	ggc	aac	tac	gtt	ctc	ttc	aat	ctc	ctg	gtg	2448
	Val	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	Val	
					805					810					815		
30	gct	atc	ctg	gta	gag	ggt	ttc	cag	gct	gag	ggt	gat	gct	aat	cgt	tcc	2496
	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Gly	Asp	Ala	Asn	Arg	Ser	
				820					825					830			
35	tgc	tct	gat	gag	gac	cag	agc	tca	tcc	aat	ttg	gag	gag	ttt	gac	aag	2544
	Cys	Ser	Asp	Glu	Asp	Gln	Ser	Ser	Ser	Asn	Leu	Glu	Glu	Phe	Asp	Lys	
			835					840					845				
	ctc	cca	gag	ggc	ctg	gac	aac	agt	aga	gat	ctc	aag	ctc	tgc	cca	ata	2592
	Leu	Pro	Glu	Gly	Leu	Asp	Asn	Ser	Arg	Asp	Leu	Lys	Leu	Cys	Pro	Ile	
		850					855					860					
40	ccc	atg	aca	ccc	aat	gga	cac	ctg	gac	cct	agc	ctc	cct	ctg	ggt	gcg	2640
	Pro	Met	Thr	Pro	Asn	Gly	His	Leu	Asp	Pro	Ser	Leu	Pro	Leu	Gly	Ala	
	865					870					875					880	
45	cat	ctg	ggt	cct	gct	ggt	acc	atg	ggt	act	gcc	ccc	cgc	ctc	tca	ctg	2688
	His	Leu	Gly	Pro	Ala	Gly	Thr	Met	Gly	Thr	Ala	Pro	Arg	Leu	Ser	Leu	
					885					890					895		
50	cag	cca	gac	ccg	gta	ctg	gtg	gcc	cta	gac	tct	cgg	aaa	agc	agt	gtc	2736
	Gln	Pro	Asp	Pro	Val	Leu	Val	Ala	Leu	Asp	Ser	Arg	Lys	Ser	Ser	Val	
				900					905					910			
55	atg	tcc	ctg	ggc	agg	atg	agc	tat	gat	cag	cga	tcc	ttg	tcc	agc	tcc	2784
	Met	Ser	Leu	Gly	Arg	Met	Ser	Tyr	Asp	Gln	Arg	Ser	Leu	Ser	Ser	Ser	
			915					920					925				
	cgg	agc	tcc	tac	tac	ggg	ccc	tgg	ggc	cgc	agt	ggg	acc	tgg	gct	agc	2832
	Arg	Ser	Ser	Tyr	Tyr	Gly	Pro	Trp	Gly	Arg	Ser	Gly	Thr	Trp	Ala	Ser	
		930					935					940					
60	cgc	cgc	tcc	agc	tgg	aac	agc	ctg	aaa	cac	aag	ccg	ccc	tca	gct	gag	2880
	Arg	Arg	Ser	Ser	Trp	Asn	Ser	Leu	Lys	His	Lys	Pro	Pro	Ser	Ala	Glu	
	945					950					955					960	
	cat	gag	tcc	tta	ctg	tct	ggg	gag	ggt	gga	ggt	agc	tgc	gtc	agg	gcc	2928

	His	Glu	Ser	Leu	Leu	Ser	Gly	Glu	Gly	Gly	Gly	Ser	Cys	Val	Arg	Ala	
					965					979					975		
5	tgt	gaa	ggc	gcc	cgg	gag	gag	gcg	cca	act	cgc	acc	gca	ccc	ctg	cat	2976
	Cys	Glu	Gly	Ala	Arg	Glu	Glu	Ala	Pro	Thr	Arg	Thr	Ala	Pro	Leu	His	
				980					985					990			
10	gct	cca	cac	gcg	cac	cac	gcg	cac	cat	gga	ccc	cac	ctg	gca	cac	cgt	3024
	Ala	Pro	His	Ala	His	His	Ala	His	His	Gly	Pro	His	Leu	Ala	His	Arg	
			995				1000					1005					
15	cac	cga	cac	cac	cgc	cgg	act	ctg	tcc	ctt	gat	acc	agg	gac	tct	gtt	3072
	His	Arg	His	His	Arg	Arg	Thr	Leu	Ser	Leu	Asp	Thr	Arg	Asp	Ser	Val	
	1010						1015					1020					
20	gac	ctg	gga	gag	ctg	gtg	ccc	gtg	gtg	ggg	gcc	cac	tca	cgg	gcc	gct	3120
	Asp	Leu	Gly	Glu	Leu	Val	Pro	Val	Val	Gly	Ala	His	Ser	Arg	Ala	Ala	
	1025					1030					1035					1040	
25	tgg	agg	ggg	gcg	ggt	cag	gcc	cct	ggg	cac	gag	gac	tgc	aat	ggc	aga	3168
	Trp	Arg	Gly	Ala	Gly	Gln	Ala	Pro	Gly	His	Glu	Asp	Cys	Asn	Gly	Arg	
				1045						1050					1055		
30	atg	ccc	aac	ata	gcc	aag	gat	gtc	ttc	acc	aag	atg	gat	gac	cgc	cgc	3216
	Met	Pro	Asn	Ile	Ala	Lys	Asp	Val	Phe	Thr	Lys	Met	Asp	Asp	Arg	Arg	
			1060						1065					1070			
35	gac	cgc	ggg	gag	gac	gag	gag	gag	atc	gac	tat	acc	ctg	tgt	ttc	cgg	3264
	Asp	Arg	Gly	Glu	Asp	Glu	Glu	Glu	Ile	Asp	Tyr	Thr	Leu	Cys	Phe	Arg	
		1075						1080					1085				
40	gtc	cgc	aag	atg	att	gat	gtg	tac	aag	ccg	gac	tgg	tgc	gaa	gtc	cgc	3312
	Val	Arg	Lys	Met	Ile	Asp	Val	Tyr	Lys	Pro	Asp	Trp	Cys	Glu	Val	Arg	
	1090						1095					1100					
45	gag	gac	tgg	tcg	gtc	tac	ctc	ttc	tcc	ccc	gag	aac	aag	ttc	cgg	atc	3360
	Glu	Asp	Trp	Ser	Val	Tyr	Leu	Phe	Ser	Pro	Glu	Asn	Lys	Phe	Arg	Ile	
	1105				1110						1115					1120	
50	ctg	tgt	cag	acc	atc	att	gct	cac	aag	ctt	ttt	gac	tac	gtg	gtc	ttg	3408
	Leu	Cys	Gln	Thr	Ile	Ile	Ala	His	Lys	Leu	Phe	Asp	Tyr	Val	Val	Leu	
				1125						1130					1135		
55	gcc	ttt	atc	ttc	ctc	aac	tgt	atc	acc	att	gct	ctg	gag	aga	ccc	cag	3456
	Ala	Phe	Ile	Phe	Leu	Asn	Cys	Ile	Thr	Ile	Ala	Leu	Glu	Arg	Pro	Gln	
			1140					1145						1150			
60	att	gaa	gct	ggt	agc	act	gag	cgc	atc	ttc	ctc	acg	gtg	tct	aac	tac	3504
	Ile	Glu	Ala	Gly	Ser	Thr	Glu	Arg	Ile	Phe	Leu	Thr	Val	Ser	Asn	Tyr	
		1155						1160					1165				
65	atc	ttc	aca	gcc	atc	ttc	gtg	ggc	gag	atg	aca	ctg	aag	gtg	gtt	tct	3552
	Ile	Phe	Thr	Ala	Ile	Phe	Val	Gly	Glu	Met	Thr	Leu	Lys	Val	Val	Ser	
	1170						1175					1180					
70	ctg	ggc	ctg	tac	ttt	ggt	gag	cag	gcg	tac	ctg	cgt	agc	agc	tgg	aat	3600
	Leu	Gly	Leu	Tyr	Phe	Gly	Glu	Gln	Ala	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	
	1185				1190						1195					1200	
75	gta	ctg	gat	ggt	ttc	ctg	gtc	ttt	gtg	tcc	atc	atc	gat	atc	gta	gtg	3648
	Val	Leu	Asp	Gly	Phe	Leu	Val	Phe	Val	Ser	Ile	Ile	Asp	Ile	Val	Val	
				1205						1210					1215		
80	tcc	gtg	gcc	tct	gct	ggg	gga	gcc	aag	att	ctg	ggg	gtc	ctc	cgg	gtc	3696

	Ser Val Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val	
	1220 1225 1230	
5	ctg cgg ctc ctg cgt acc tta cgt cct ttg agg gtt atc agc cgg gcc Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala	3744
	1235 1240 1245	
10	cct ggg ctg aag ctg gtg gta gag acg ctc atc tcc tcc ctc aag ccc Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro	3792
	1250 1255 1260	
15	att ggg aac atc gtc ctc atc tgc tgt gcc ttc ttc atc atc ttc ggc Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly	3840
	1265 1270 1275 1280	
	atc ctg ggg gtg cag ctt ttc aaa ggc aag ttc tac cat tgt ttg gga Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly	3888
	1285 1290 1295	
20	gtg gac acc cga aac atc acc aac cga tct gac tgc gtg gcg gcc aac Val Asp Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Val Ala Ala Asn	3936
	1300 1305 1310	
25	tac cgc tgg gtg cat cac aaa tac aac ttt gac aac ctg ggc cag gca Tyr Arg Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala	3984
	1315 1320 1325	
30	ttg atg tcc ctc ttt gtc ttg gcc tcc aag gac ggc tgg gtg aac atc Leu Met Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile	4032
	1330 1335 1340	
35	atg tat aat gga tta gat gct gtt gct gtg gac cag cag cca gtg acg Met Tyr Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr	4080
	1345 1350 1355 1360	
	aac cac aac ccc tgg atg cta ctg tac ttc att tgc ttc ctg ctc atc Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile	4128
	1365 1370 1375	
40	gtc agc ttc ttt gtg ctc aac atg ttt gtg ggc gtg gtc gtg gag aac Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn	4176
	1380 1385 1390	
45	ttc cac aag tgc cgg cag cac cag gag gct gag gag gcg cgg agg cgt Phe His Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg	4224
	1395 1400 1405	
50	gag gag aaa cgg ctg cgg cgc ctg gaa aag aag cgc cgt aag gct cag Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln	4272
	1410 1415 1420	
55	agg ctg ccc tac tat gct acc tac tgt ccc aca agg ctg ctc atc cac Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys Pro Thr Arg Leu Leu Ile His	4320
	1425 1430 1435 1440	
	tcc atg tgc acc agc cac tac ctg gac atc ttc att acc ttc atc atc Ser Met Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile	4368
	1445 1450 1455	
60	tgc ctc aat gtt gtc acc atg tcc ctg gag cac tac aac cag cct aca Cys Leu Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr	4416
	1460 1465 1470	
	tcc cta gag aca gcc ctt aag tac tgc aac tac atg ttc acc act gtc	4464





Pro Cys Pro Cys Pro Cys Pro Cys Ala Gly Pro Arg Leu Pro Thr Ser  
 1730 1735 1740  
 5 tca cct ggg gct ccg ggg cga gga tgg gga ggg gca ggt gct gga ggc 5280  
 Ser Pro Gly Ala Pro Gly Arg Gly Ser Gly Gly Ala Gly Ala Gly Gly  
 1745 1750 1755 1760  
 10 gac acc gag agt cac ctg tgc cgg cac tgc tat tct cca gcc cag gag 5328  
 Asp Thr Glu Ser His Leu Cys Arg His Cys Tyr Ser Pro Ala Gln Glu  
 1765 1770 1775  
 acc ctg tgg ctg gac agc gtc tct tta atc atc aag gac tcc ttg gag 5376  
 Thr Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys Asp Ser Leu Glu  
 1780 1785 1790  
 15 ggg gag ctg acc atc att gac aac ctg tct ggg tcc gtc ttc cac cac 5424  
 Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser Val Phe His His  
 1795 1800 1805  
 20 tac gcc tca cct gac ggc tgt ggc aag tgt cac cat gac aag caa gag 5472  
 Tyr Ala Ser Pro Asp Gly Cys Gly Lys Cys His His Asp Lys Gln Glu  
 1810 1815 1820  
 25 aca ggt ctt cat cca tcc tgc tgg ggg atg acc 5505  
 Thr Gly Leu His Pro Ser Cys Trp Gly Met Thr  
 1825 1830 1835  
 30 <210> 13  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens  
 <400> 13  
 35 Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu  
 1 5 10 15  
 Lys Met Ala

40

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/23161

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C07K16/28 C12N5/10 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 04144 A (NEUREX CORP) 9 February 1995	1,2,7, 10-18, 20-22
Y	see abstract; claims 1-10 ---	3,19
X	NOONEY JM (REPRINT) ET AL: "Identifying neuronal non-L Ca2+ channels - more than stamp collecting?" TRENDS IN PHARMACOLOGICAL SCIENCES, 10-1997, 18, 363-371, XP002093637 see page 369, right-hand column - page 370, right-hand column --- -/--	1,2, 10-16, 20-22

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

16 February 1999

Date of mailing of the international search report

09/03/1999

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl.  
Fax: (+31-70) 340-3016

Authorized officer

Gurdjian, D

# INTERNATIONAL SEARCH REPORT

Intern    al Application No

PCT/US 98/23161

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ERTEL S I ET AL: "Low-voltage-activated T-type Cachannels" TRENDS IN PHARMACOLOGICAL SCIENCES, vol. 18, no. 2, February 1997, page 37-42 XP004055849 see page 39, left-hand column, paragraph 4 - page 40, middle column, paragraph 1; table 1 ---	1,2, 10-16, 20-22
X	DZHURA IO ET AL: "Characterization of hypothalamic low-voltage-activated Ca channels based on their functional expression in Xenopus oocytes." NEUROSCIENCE, FEB 1996, 70 (3) P729-38, XP002093638 UNITED STATES see the whole document ---	1,2, 10-18, 20-22
Y	WILSON R ET AL: "2.2 MB OF CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III OF C ELEGANS" NATURE, vol. 368, 3 March 1994, pages 32-38, XP002910426 see abstract ---	3,19
Y	& EMBL DATABASE Accession number q18840 WILSON R. ET AL. 1996 see the whole document ---	3,19
A	WO 93 04083 A (SALK INST BIOTECH IND) 4 March 1993 see abstract; claims 1-39 ---	1-22
P,X	PEREZ-REYES E ET AL: "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel 'see comments!'" NATURE, FEB 26 1998, 391 (6670) P896-900, XP002093639 ENGLAND see the whole document ---	1-15, 20-22
P,X	CRIBBS LL ET AL: "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family." CIRC RES, JUL 13 1998, 83 (1) P103-9, XP002093640 UNITED STATES see the whole document -----	1-22

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/23161

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9504144 A	09-02-1995	EP 0778890 A	18-06-1997
		JP 9501051 T	04-02-1997
WO 9304083 A	04-03-1993	US 5429921 A	04-07-1995
		AU 677571 B	01-05-1997
		AU 2495792 A	16-03-1993
		CA 2113203 A	04-03-1993
		EP 0598840 A	01-06-1994
		JP 6509717 T	02-11-1994
		US 5846757 A	08-12-1998
		US 5851824 A	22-12-1998
		US 5792846 A	11-08-1998

**THIS PAGE BLANK (USPTO)**